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Matches 11; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 3 RQKPPSPKPNDFHFEVFNFPVPCISNNPTCWA 36
  | : | | : : | | : | | |
Db 794 RSEAPSWEQHCWRTGEGGFVCCCLCIQGPVCA 827

RESULT 3
US-09-724-676-57037
; Sequence 57037, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57037
; LENGTH: 836
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-57037

Query Match 19.8%; Score 57; DB 5; Length 836;
Best Local Similarity 32.4%; Pred. No. 23;
Matches 11; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 3 RQKPPSPKPNDFHFEVFNFPVPCISNNPTCWA 36
  | : | | : : | | : | | |
Db 794 RSEAPSWEQHCWRTGEGGFVCCCLCIQGPVCA 827

RESULT 4
US-09-724-676-57038
; Sequence 57038, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57038
; LENGTH: 836
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-57038

Query Match 19.8%; Score 57; DB 5; Length 836;
Best Local Similarity 32.4%; Pred. No. 23;
Matches 11; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 3 RQKPPSPKPNDFHFEVFNFPVPCISNNPTCWA 36
  | : | | : : | | : | | |
Db 794 RSEAPSWEQHCWRTGEGGFVCCCLCIQGPVCA 827

RESULT 5
US-09-724-676-57039
; Sequence 57039, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57039
; LENGTH: 836
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-57039

Query Match 19.8%; Score 57; DB 5; Length 836;
Best Local Similarity 32.4%; Pred. No. 23;
Matches 11; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 3 RQKPPSPKPNDFHFEVFNFPVPCISNNPTCWA 36
  | : | | : : | | : | | |
Db 794 RSEAPSWEQHCWRTGEGGFVCCCLCIQGPVCA 827

RESULT 6
US-09-724-676-57040
; Sequence 57040, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57040
; LENGTH: 836
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-57040

Query Match 19.8%; Score 57; DB 5; Length 836;
Best Local Similarity 32.4%; Pred. No. 23;
Matches 11; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 3 RQKPPSPKPNDFHFEVFNFPVPCISNNPTCWA 36
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Db 794 RSEAPSWEQHCWRTGEGGFVCCCLCIQGPVCA 827

RESULT 7
US-09-724-676-57041
; Sequence 57041, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57041
; LENGTH: 836
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-57041

Query Match 19.8%; Score 57; DB 5; Length 836;
Best Local Similarity 32.4%; Pred. No. 23;
Matches 11; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 3 RQKPPSPKPNDFHFEVFNFPVPCISNNPTCWA 36
  | : | | : : | | : | | |
Db 794 RSEAPSWEQHCWRTGEGGFVCCCLCIQGPVCA 827

RESULT 8
US-09-724-676-57071
; Sequence 57071, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
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Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
19.8%	32.4%	57	5	836	19	4	0
Matches	Matches	Conservative					
3	794	3	794	3	794	3	794
RQNKPPSKPNNDFHFEVFNVP	RQNKPPSKPNNDFHFEVFNVP	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA
36	36	36	36	36	36	36	36
DB	DB	DB	DB	DB	DB	DB	DB
794	794	794	794	794	794	794	794
RSEAPSWEQHCWRTGEGGFVCC	RSEAPSWEQHCWRTGEGGFVCC	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA
827	827	827	827	827	827	827	827
US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071
Query Match	Best Local Similarity	Score <td>DB <td>Length <td>Indels <td>Mismatches <td>Gaps </td></td></td></td></td>	DB <td>Length <td>Indels <td>Mismatches <td>Gaps </td></td></td></td>	Length <td>Indels <td>Mismatches <td>Gaps </td></td></td>	Indels <td>Mismatches <td>Gaps </td></td>	Mismatches <td>Gaps </td>	Gaps
19.8%	32.4%	57	5	836	19	4	0
Matches	Matches	Conservative					
3	794	3	794	3	794	3	794
RQNKPPSKPNNDFHFEVFNVP	RQNKPPSKPNNDFHFEVFNVP	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA
36	36	36	36	36	36	36	36
DB	DB	DB	DB	DB	DB	DB	DB
794	794	794	794	794	794	794	794
RSEAPSWEQHCWRTGEGGFVCC	RSEAPSWEQHCWRTGEGGFVCC	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA
827	827	827	827	827	827	827	827
US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071
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19.8%	32.4%	57	5	836	19	4	0
Matches	Matches	Conservative					
3	794	3	794	3	794	3	794
RQNKPPSKPNNDFHFEVFNVP	RQNKPPSKPNNDFHFEVFNVP	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA
36	36	36	36	36	36	36	36
DB	DB	DB	DB	DB	DB	DB	DB
794	794	794	794	794	794	794	794
RSEAPSWEQHCWRTGEGGFVCC	RSEAPSWEQHCWRTGEGGFVCC	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA
827	827	827	827	827	827	827	827
US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071
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19.8%	32.4%	57	5	836	19	4	0
Matches	Matches	Conservative					
3	794	3	794	3	794	3	794
RQNKPPSKPNNDFHFEVFNVP	RQNKPPSKPNNDFHFEVFNVP	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA	CSICSNNPTCWA
36	36	36	36	36	36	36	36
DB	DB	DB	DB	DB	DB	DB	DB
794	794	794	794	794	794	794	794
RSEAPSWEQHCWRTGEGGFVCC	RSEAPSWEQHCWRTGEGGFVCC	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA	CLCIQGPVCWA
827	827	827	827	827	827	827	827
US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071	US-09-724-676-57071
Query Match	Best Local Similarity	Score <td>DB <td>Length <td>Indels <td>Mismatches </td></td></td></td>	DB <td>Length <td>Indels <td>Mismatches </td></td></td>	Length <td>Indels <td>Mismatches </td></td>	Indels <td>Mismatches </td>	Mismatches	

RESULT 14

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US-09-724-676-57108
; Sequence 57108, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ.ID.NO 57108
; LENGTH: 836
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-57108

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Query Match 19.8%; Score 57; DB 5; Length 836;
Best Local Similarity 32.4%; Pred. No. 23;
Matches 11; Conservative 4; Mismatches 19; Indels

Qy 3 RQNKPPSKPNNDPHFEVFNFPVCSICSNNPTCWA 36
| - : || : : || : | - |||
Db 794 RSEAPSWEQHCWRTGEGGFVCCCLCIQGPVCWA 827

RESULT. 15

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US-09-724-676-57110
; Sequence 57110, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57110
; LENGTH: 836
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-57110

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Query Match      19.8%; Score 57; DB 5; Length 836;
Best Local Similarity 32.4%; Pred. No. 23;
Matches 11; Conservative 4; Mismatches 19; Indels
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QY | 3 RQNKPPSKPNNDFHFEVFNVPSCISNNTCWA 36
| : || : : || : : || : : ||
Db 794 RSEAPSWEOHCWRTGEGGFVCCCLCIOGPVCWA 827

Search completed: November 22, 2002, 14:30:05
Job time : 12 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 14:25:47 ; Search time 141 Seconds
(without alignments)
224.056 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KORQKPPSPNNDHFHFEV.....NNPTCWAICKRIPNKKPKKK 49

Scoring table: BLOSUM62

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Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	288	100.0	49	16	US-09-202-035-42
6	288	100.0	49	16	US-09-202-035-43

7	288	100.0	298	27	US-60-208-701-2	Sequence 2, Appli
8	285	99.0	49	16	US-09-202-035-2	Sequence 2, Appli
9	285	99.0	49	16	US-09-202-035-3	Sequence 3, Appli
10	285	99.0	49	16	US-09-202-035-5	Sequence 5, Appli
11	285	99.0	49	16	US-09-202-035-6	Sequence 6, Appli
12	285	99.0	49	16	US-09-202-035-7	Sequence 7, Appli
13	285	99.0	49	16	US-09-202-035-8	Sequence 8, Appli
14	285	99.0	59	20	US-09-647-309A-40	Sequence 40, Appli
15	285	99.0	61	20	US-09-647-309A-38	Sequence 38, Appli
16	285	99.0	101	18	US-09-462-918C-43	Sequence 43, Appli
17	285	99.0	101	20	US-09-647-309A-4	Sequence 4, Appli
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20	285	99.0	232	12	US-08-896-442-4	Sequence 4, Appli
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22	285	99.0	232	18	US-09-462-816-4	Sequence 4, Appli
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42	285	99.0	298	16	US-09-272-262-2	Sequence 2, Appli
43	285	99.0	298	18	US-09-462-816-2	Sequence 2, Appli
44	285	99.0	298	18	US-09-479-240-8	Sequence 8, Appli
45	285	99.0	452	24	US-10-088-720-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-202-035-1
; Sequence 1, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of Respiratory Syncytial Virus
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-1

Query Match 100.0%; Score 288; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORQKPPSPNNDHFHFEVFNFPVCSICSNPTCWAICKRIPNKKPKKK 49
DB 1 KORQKPPSPNNDHFHFEVFNFPVCSICSNPTCWAICKRIPNKKPKKK 49

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RESULT 2
; Sequence 32, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; EARLIER FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: respiratory syncytial virus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (49)
; OTHER INFORMATION: amidation
US-09-202-035-32
Query Match 100.0%; Score 288; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORQKPPSKPNNDHFVEFVPCSCSNNPTCWAICKRIPNKKPGKK 49
Db 1 KORQKPPSKPNNDHFVEFVPCSCSNNPTCWAICKRIPNKKPGKK 49
RESULT 3
; Sequence 36, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; EARLIER FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: acetylation
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (49)
; OTHER INFORMATION: amidation
US-09-202-035-36
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Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORQKPPSKPNNDHFVEFVPCSCSNNPTCWAICKRIPNKKPGKK 49
Db 1 KORQKPPSKPNNDHFVEFVPCSCSNNPTCWAICKRIPNKKPGKK 49
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; Sequence 40, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; EARLIER FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: benzoyl benzylamide derivatisation
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (49)
; OTHER INFORMATION: amidation
US-09-202-035-40
Query Match 100.0%; Score 288; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORQKPPSKPNNDHFVEFVPCSCSNNPTCWAICKRIPNKKPGKK 49
Db 1 KORQKPPSKPNNDHFVEFVPCSCSNNPTCWAICKRIPNKKPGKK 49
```

```
US-09-202-035-40
; Sequence 40, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; EARLIER FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: fluorescein isothiocarbamyl beta-alanine
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (49)
; OTHER INFORMATION: amidation
US-09-202-035-40
Query Match 100.0%; Score 288; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORQKPPSKPNNDHFVEFVPCSCSNNPTCWAICKRIPNKKPGKK 49
Db 1 KORQKPPSKPNNDHFVEFVPCSCSNNPTCWAICKRIPNKKPGKK 49
RESULT 5
; Sequence 42, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; EARLIER FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: benzoyl benzylamide derivatisation
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (49)
; OTHER INFORMATION: amidation
US-09-202-035-42
Query Match 100.0%; Score 288; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORQKPPSKPNNDHFVEFVPCSCSNNPTCWAICKRIPNKKPGKK 49
Db 1 KORQKPPSKPNNDHFVEFVPCSCSNNPTCWAICKRIPNKKPGKK 49
```

[illegible]

```

RESULT 6
US-09-202-035-43
; Sequence 43, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; TITLE OF INVENTION: Respiratory Syncytial Virus
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: biotinyl amide derivatization
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (49)
; OTHER INFORMATION: amidation
US-09-202-035-43

```

```

Query Match      100.0%; Score 288; DB 16; Length 49;
Best local Similarity 100.0%; Pred. No. 1e-25;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORONKPPSPNNDFHFEVFNVPSCISNNPTCWAICKRIPNKKPKKK 49
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 KORONKPPSPNNDFHFEVFNVPSCISNNPTCWAICKRIPNKKPKKK 49
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```

RESULT 7
US-60-208-701-2
; Sequence 2, Application US/60208701
; GENERAL INFORMATION:
; APPLICANT: Portner, Allen
; APPLICANT: Takimoto, Toru
; TITLE OF INVENTION: VACCINE AND GENE THERAPY VECTOR AND METHODS OF USE
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 1340-1-030P
; CURRENT APPLICATION NUMBER: US/60/208,701
; CURRENT FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Paramyxoviridae pneumovirinae
US-60-208-701-2
; ORGANISM: pneumovirus respiratory syncy

```

```

Query Match      100.0%; Score 288; DB 27; Length 298;
Best Local Similarity 100.0%; Pred. No. 6.1e-25;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKNNDFHFVFVFPVPCISCNPTCWAICKRIPNKKPGKK 49
   |||||
Db 149 KORONKPPSKNNDFHFVFVFPVPCISCNPTCWAICKRIPNKKPGKK 197
   |||||

RESULT 8

```

```

US-09-202-035-2
; Sequence 2, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; TITLE OF INVENTION: Respiratory Syncytial Virus
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-2

```

```

Query Match      99.08; Score 285; DB 16; Length 49;
Best local Similarity 96.08; Pred. No. 2.3e-25;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KQRONKPPSKNNDFHEFVFNFVPCSCSNNPTCWAICKRIPNKKPKKK 49
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 KQRONKPPNNDNFHFVFNFVPCSCSCSNNPTCWAICKRIPNKKPKKK 49
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```

RESULT 9
US-09-202-035-3
: Sequence 3, Application US/09202035
: GENERAL INFORMATION:
: APPLICANT: Jeffrey John Gorman
: TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
: Respiratory Syncytial Virus
: FILE REFERENCE: 41585200100
: CURRENT APPLICATION NUMBER: US/09/202,035
: CURRENT FILING DATE: 1998-12-17
: EARLIER APPLICATION NUMBER: PCT/AU97/00351
: EARLIER FILING DATE: 1997-06-04
: EARLIER APPLICATION NUMBER: AU PO 0265
: EARLIER FILING DATE: 1996-06-05
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3
: LENGTH: 49
: TYPE: PRT
: ORGANISM: respiratory syncytial virus
US-09-202-035-3

```

Query Match	99.0%	Score 285;	DB 16;	Length 49;
Best Local Similarity	98.0%;	Pred. No. 2.3e-25;		
Matches 48;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	KQRQNKPPSKNPDPHFHFVFVPCISCSNNPTCWAICKRIPNKKPKGKK	49	
Db	1	KORQNKPPSKNPDPHFHFVFVPCISCSNNPTCWAICKRIPNKKPKGKK	49	

```

RESULT 10
US-09-202-035-5
; Sequence 5, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; TITLE OF INVENTION: Respiratory Syncytial Virus
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04

```

US-09-202-035-5

US-09-202-033-8
; Sequence 8, Application US/09202035
; GENERAL INFORMATION:

```

: APPLICANT: Jeffrey John Gorman
:
: TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G Of
:
: TITLE OF INVENTION: Respiratory Syncytial Virus
:
: FILE REFERENCE: 415852000100
:
: CURRENT APPLICATION NUMBER: US/09/202,035
:
: CURRENT FILING DATE: 1998-12-17
:
: EARLIER APPLICATION NUMBER: PCT/AU97/00351
:

```

```

: APPLICANT:
: TITLE OF INV:
: TITLE OF INV:
: FILE REFEREN:
: CURRENT APPL:
: CURRENT FILL:
: EARLIER APPL:
: EARLIER FILL:
: EARLIER APPL:
: EARLIER FILL:
: NUMBER OF SE:
: SOFTWARE: Pa
: SEQ ID NO 8
: LENGTH: 49
: TYPE: PRT
: ORGANISM: r
US-09-202-035-8

```

```
Query Match      99.0%; Score 285; DB 16; Length 49;
Best Local Similarity 98.0%; Pred. No. 2.3e-25;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 14
US-09-647-309A-40
; Sequence 40, Ap

```

: GENERAL INFORMATION:
: APPLICANT: Pierre Fabre Medicament
: TITLE OF INVENTION: USE OF ACTIVE P40 CONJUGATES FOR NASAL DELIVERY
: FILE REFERENCE: D17084
: CURRENT APPLICATION NUMBER: US/09/647,309A
: CURRENT FILING DATE: 2002-02-28
: PRIOR APPLICATION NUMBER: FR 98 03814
:

```

APPLICANT: PIERRE FABRE MEDICAMENT
TITLE OF INVENTION: USE OF ACTIVE P40 CONJUGATES FOR NASAL DELIVERY

; FILE REFERENCE: D17064
; CURRENT APPLICATION NUMBER: US/09/647,309A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: FR 98 03814
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 38
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Respiratory syncytial Virus (RSV)
US-09-647-309A-38

Query Match 99.0%; Score 285; DB 20; Length 61;
Best Local Similarity 98.0%; Pred. No. 2.9e-25;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KORQNKPPSKPNDFEFVFNVPSCSICSNPTCWAICKRIPIKPKGKK 49
Db 10 KORQNKPPKNDFEFVFNVPSCSICSNPTCWAICKRIPIKPKGKK 58

Search completed: November 22, 2002, 14:29:48
Job time : 142 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 14:24:42 ; Search time 18 Seconds
(without alignments)
261.699 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KQRQKPPSKPNDFHFEV.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	288	100.0	298	1	MGNZ
2	285	99.0	297	2	major surface glycoprotein
3	285	99.0	297	2	attachment protein
4	285	99.0	297	2	attachment protein
5	285	99.0	298	1	major surface glycoprotein - Human
6	285	99.0	298	2	attachment protein
7	280	97.2	298	2	attachment protein
8	279	96.9	297	2	attachment protein
9	273	94.8	297	2	attachment protein
10	190	66.0	292	1	MGN18
11	190	66.0	292	1	MGN260
12	83.5	29.0	257	1	MGN28
13	80	27.8	263	2	major surface glycoprotein G - b
14	79	27.4	250	2	glycoprotein G - b
15	77.5	26.9	248	2	glycoprotein G - b
16	77.5	26.9	263	2	glycoprotein G - o
17	77.5	26.9	263	2	attachment glycoprotein
18	66.5	23.1	274	2	diaminopimelate ep
19	66.5	23.1	274	2	diaminopimelate ep
20	66.5	23.1	275	1	AC0919
21	66.5	23.1	275	1	S01913
22	66.5	23.1	275	2	C91221
23	64	22.2	37	2	F86067
24	63.5	22.0	274	2	charybdotoxin 2
25	63	21.9	1861	2	diaminopimelate ep
26	62	21.5	37	2	microtubule-associ
27	62	21.5	290	2	charybdotoxin 1 [v
28	61	21.2	375	2	diaminopimelate ep
29	60.5	21.0	1506	2	A/G-specific adeni
					hypothetical prote

ALIGNMENTS

RESULT 1

MGNZ

major surface glycoprotein G - human respiratory syncytial virus

C:Species: human respiratory syncytial virus

C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 24-Sep-1999

C:Accession: A94048; A93599; A04039

R:Wertz, G.W.; Collins, P.T.; Huang, X.; Gruber, C.; Levine, S.; Ball, L.A.

Proc. Natl. Acad. Sci. U.S.A. 82, 4075-4079, 1985

A>Title: Nucleotide sequence of the G protein gene of human respiratory syncytial vlr

A:Reference number: A94048; MUID:85216636; PMID:3858865

A:Accession: A94048

A:Molecule type: mRNA

A:Residues: 1-298 <WER>

A:Cross-references: GB:M11486; GB:K01459; GB:K02719; GB:K03348; GB:K03349; GB:M11217;

7.1; PID:g333932

A>Note: residues 207-298 are identical with residues 376-467 of the nucleocapsid prot

A>Note: this protein may carry 40-80 separate O-linked carbohydrate chains distribute

R:State, M.; Colligan, J.E.; Elango, N.; Norrby, E.; Venkatesan, S.

Nucleic Acids Res. 13, 7795-7812, 1985

A>Title: Respiratory syncytial virus envelope glycoprotein (G) has a novel structure.

A:Reference number: A93599; MUID:86067198; PMID:406997

A:Accession: A93599

A:Molecule type: mRNA

A:Residues: 1-298 <SAT>

A:Cross-references: GB:X03149; NID:g60997; PID:CAA26928.1; PID:g60998

C:Superfamily: respiratory syncytial virus major surface glycoprotein G

C:Keywords: glycoprotein; transmembrane protein

F:38-66/Domain: transmembrane #status predicted <TNM>

F:85,135,237,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 288; DB 1; Length 298;

Best Local Similarity 100.0%; Pred. No. 1.7e-26;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy .1 KQRQKPPSKPNDFHFEVFNFCSTCSNNPTCWAICKRIPNKKPGKK 49

|||||

Db 149 KQRQKPPSKPNDFHFEVFNFCSTCSNNPTCWAICKRIPNKKPGKK 197

|||||

RESULT 2

JQ1205

attachment protein - human respiratory syncytial virus (strain RSB1734)

N:Alternate names: G protein

C:Species: human respiratory syncytial virus

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997

C:Accession: JQ1205

R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.

J. Gen. Virol. 72, 2091-2096, 1991

A>Title: Identification of variable domains of the attachment (G) protein of subgroup

A:Reference number: JQ1204; MUID:91374005; PMID:1895054

A:Accession: JQ1205

A:Molecule type: mRNA

```
A:Residues: 1-297 <CAN>
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract il
idren and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,251,273/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      99.0%; Score 285; DB 2; Length 297;
Best Local Similarity 98.0%; Pred. No. 3.9e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPKPNDFHFEVFPVCSICSNNTCWAICKRIPNKKPGKK 49
Db 149 KORQNKPPKPNDFHFEVFPVCSICSNNTCWAICKRIPNKKPGKR 197

RESULT 3
JQ1204
attachment protein - human respiratory syncytial virus (strain RSB642)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1204
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup A
A:Reference number: JQ1204; MUID:91374005; PMID:1895054
A:Accession: JQ1204
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract il
idren and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,144,237,273/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      99.0%; Score 285; DB 2; Length 297;
Best Local Similarity 98.0%; Pred. No. 3.9e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPKPNDFHFEVFPVCSICSNNTCWAICKRIPNKKPGKK 49
Db 149 KORQNKPPKPNDFHFEVFPVCSICSNNTCWAICKRIPNKKPGKR 197

RESULT 4
JQ1208
attachment protein - human respiratory syncytial virus (strain RSB6256)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1208
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup A
A:Reference number: JQ1204; MUID:91374005; PMID:1895054
A:Accession: JQ1208
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract il
idren and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predicte
```

RESULT 5
MNZRL

major surface glycoprotein G - human respiratory syncytial virus (strain Long)
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C:Accession: A32703; S12279
R:Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A:Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and
A:Reference number: A32703; MUID:87289657; PMID:2441388

A:Accession: A32703
A:Molecule type: mRNA
A:Residues: 1-298 <JOH>
A:Cross-references: GB:M17212; NID:G333940; PIDN:AAA47411.1; PID:G333941
R:Garcia-Barreno, B.; Portela, A.; Delgado, T.; Lopez, J.A.; Melero, J.A.
EMBO J. 9, 4181-4187, 1990
A:Title: Frame shift mutations as a novel mechanism for the generation of neutraliza-

A:Reference number: S12279; MUID:91065351; PMID:2249671
A:Accession: S12279
A:Molecule type: mRNA
A:Residues: 1-298 <GAR>
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:41-63/Domain: transmembrane #status predicted <TM>
F:85,103,135,179,237,250,251,273,294/Binding site: carbohydrate (Asn) (covalent) #st-

Query Match 99.0%; Score 285; DB 1; Length 298;
Best Local Similarity 98.0%; Pred. No. 3.9e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPKPNDFHFEVFPVCSICSNNTCWAICKRIPNKKPGKK 49
Db 149 KORQNKPPKPNDFHFEVFPVCSICSNNTCWAICKRIPNKKPGKK 197

RESULT 6
JC5680

protein - Human respiratory syncytial virus
C:Species: Human respiratory syncytial virus
C:Date: 11-Nov-1997 #sequence_revision 11-Nov-1997 #text_change 26-Feb-1998
C:Accession: JC5680
R:Geng, X.; Wang, Z.; Qian, Y.; Zhu, R.; Deng, J.; Du, J.; Zhu, Z.
Chinese J. Virol. 12, 317-322, 1996
A:Title: Molecular analysis of G protein gene of a respiratory syncytial virus strain

A:Reference number: JC5680
A:Accession: JC5680
A:Molecule type: mRNA
A:Residues: 1-298 <GEN>
A:Experimental source: strain B79
A:Note: the authors translated the codon TTT for residue 165 and 170 as Glu, TTC for
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
F:1-38/Domain: intracellular #status predicted <INT>
F:39-66/Domain: transmembrane #status predicted <TM>
F:67-298/Domain: extracellular #status predicted <EXC>

Query Match 99.0%; Score 285; DB 2; Length 298;
Best Local Similarity 98.0%; Pred. No. 3.9e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPKPNDFHFEVFPVCSICSNNTCWAICKRIPNKKPGKK 49
Db 149 KORQNKPPKPNDFHFEVFPVCSICSNNTCWAICKRIPNKKPGKK 197

RESULT 7
JQ1207

attachment protein - human respiratory syncytial virus (strain RSB6190)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1207
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.

```
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup A
A:Reference number: JQ1204; MUID:91374005; PMID:1895054
A:Accession: JQ1207
A:Molecule type: mRNA
A:Residues: 1-298 <CAN>
A:Note: The authors translated the codon ACC for residue 4 as Asn and ACC for residue 22
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract il
children and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,250,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 97.2%; Score 280; DB 2; Length 298;
Best Local Similarity 95.9%; Pred. No. 1.5e-25;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORQKPPSKPNDFHFEVFPVCSICSNNTPTCWAICKRIPNKKPGKK 49
DB 149 KORQKPPNKPNDHFEVFPVCSICSNNTPTCWAICKRIPNKKPGKK 197
RESULT 8
JQ1206
attachment protein - human respiratory syncytial virus (strain RSB5857)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1206
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup A
A:Reference number: JQ1204; MUID:91374005; PMID:1895054
A:Accession: JQ1206
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract il
children and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 96.9%; Score 279; DB 2; Length 297;
Best Local Similarity 95.9%; Pred. No. 2e-25;
Matches 47; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KORQKPPSKPNDFHFEVFPVCSICSNNTPTCWAICKRIPNKKPGKK 49
DB 149 KORQKPPNKPNDHFEVFPVCSICSNNTPTCWAICKRIPNKKPGKK 197
RESULT 9
JQ1209
attachment protein - human respiratory syncytial virus (strain RSB6614)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1209
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup A
A:Reference number: JQ1204; MUID:91374005; PMID:1895054
A:Accession: JQ1209
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract il
er children and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 94.8%; Score 273; DB 2; Length 297;
Best Local Similarity 93.9%; Pred. No. 1e-24;
```

```
Matches 46; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 KORQKPPSKPNDFHFEVFPVCSICSNNTPTCWAICKRIPNKKPGKK 49
DB 149 KORQKPPNKPNDHFEVFPVCSICSNNTPTCWAICKRIPNKKPGKK 197
RESULT 10
MGN218
major surface glycoprotein G - human respiratory syncytial virus (strain 18537)
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C:Accession: B32703
R:Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A:Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and
A:Reference number: A32703; MUID:87289657; PMID:2441388
A:Accession: B32703
A:Molecule type: mRNA
A:Residues: 1-292 <JOH>
A:Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1; PID:g333943
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:41-63/Domain: transmembrane #status predicted <TMN>
F:81,86,100/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 66.0%; Score 190; DB 1; Length 292;
Best Local Similarity 65.3%; Pred. No. 5.7e-15;
Matches 32; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
QY 1 KORQKPPSKPNDFHFEVFPVCSICSNNTPTCWAICKRIPNKKPGKK 49
DB 149 KRSKNPPKPKDDYHFEVFPVCSICGNQLCKSICKTIPSNKPKKK 197
RESULT 11
MGN260
major surface glycoprotein G - human respiratory syncytial virus (strain 8/60)
N:Alternate names: attachment glycoprotein G
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: A37077
R:Sullender, W.M.; Anderson, K.; Wertz, G.W.
Virology 178, 195-203, 1990
A:Title: The respiratory syncytial virus subgroup B attachment glycoprotein: analysis
gous subgroup virus challenge.
A:Reference number: A37077; MUID:90357765; PMID:1697126
A:Accession: A37077
A:Molecule type: mRNA
A:Residues: 1-292 <SUL>
A:Cross-references: EMBL:M55633; NID:g333944; PIDN:AAA47413.1; PID:g333945
C:Genetics:
A:Gene: G
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:45-63/Domain: transmembrane #status predicted <TMN>
F:81,86,100,230,290/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 66.0%; Score 190; DB 1; Length 292;
Best Local Similarity 65.3%; Pred. No. 5.7e-15;
Matches 32; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
QY 1 KORQKPPSKPNDFHFEVFPVCSICSNNTPTCWAICKRIPNKKPGKK 49
DB 149 KRSKNPPKPKDDYHFEVFPVCSICGNQLCKSICKTIPSNKPKKK 197
RESULT 12
MGN2BR
major surface glycoprotein G - bovine respiratory syncytial virus (strain 391-2)
N:Alternate names: attachment glycoprotein G
C:Species: bovine respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
```

C;Accession: A36408
J;erch, R.A.; Anderson, K.; Wertz, G.W.
J. Virol. 64, 5559-5565, 1990
A;Title: Nucleotide sequence analysis and expression from recombinant vectors demonstrated Y syncytial virus.
A;Reference number: A36408; MUID:91012801; PMID:2214024
A;Accession: A36408
A;Molecule type: mRNA
A;Residues: 1-257 <LER>
A;Cross-references: GB:M58307; NID:g210830; PIDN:AAA42810.1; PID:g210831
C;Genetics:
A;Gene: G
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;45-62/Domain: transmembrane #status predicted <TMN>
F;3,85,127,149,233,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.0%; Score 83.5; DB 1; Length 257;
Best Local Similarity 29.6%; Pred. No. 0.017;
Matches 16; Conservative 9; Mismatches 16; Indels 13; Gaps 2;

QY | 6 KPSPKPNNDP-----HFEVNFVPCISNNPTCWAIC----KRIPNKKP 46
| | | | | : : : : | | | | | : : : : | | : : |
Db | 145 KPINSGSIPPHQHNNHNSQTLFVPCSTCEGNLACLSLCHIEIETAPSRAP 198

RESULT 13
JQ2284
glycoprotein G - bovine respiratory syncytial virus (isolate A51908)
C;Species: bovine respiratory syncytial virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: JQ2284
R;Mallipeddi, S.K.; Samal, S.K.
J. Gen. Virol. 74, 2001-2004, 1993
A;Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial virus
A;Reference number: JQ2284; MUID:93389461; PMID:8376974
A;Accession: JQ2284
A;Molecule type: mRNA
A;Residues: 1-263 <NAL>
A;Experimental source: isolate A51908
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;1-38/Domain: intracellular #status predicted <CYT>
F;39-66/Domain: transmembrane #status predicted <TMN>
F;67-263/Domain: extracellular #status predicted <EXT>
F;127,163,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.8%; Score 80; DB 2; Length 263;
Best Local Similarity 29.8%; Pred. No. 0.044;
Matches 14; Conservative 9; Mismatches 20; Indels 4; Gaps 1;

QY | 4 QNKPPSKPNNDPHEVNFVPCISNNPTCWAIC----KRIPNKKP 46
| | | | | : : : : | | | | | : : : : | | : : |
Db | 152 ESNPPHNDHNSQTLFVPCSTCEGNPACSPICQIGLERAPSRAP 198

RESULT 14
PQ0768
glycoprotein G - bovine respiratory syncytial virus (isolate FS-1) (fragment)
C;Species: bovine respiratory syncytial virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: PQ0768
R;Mallipeddi, S.K.; Samal, S.K.
J. Gen. Virol. 74, 2001-2004, 1993
A;Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial virus
A;Reference number: JQ2284; MUID:93389461; PMID:8376974
A;Accession: PQ0768
A;Molecule type: mRNA
A;Residues: 1-250 <NAL>
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;1-31/Domain: intracellular #status predicted <INT>
F;32-59/Domain: transmembrane #status predicted <TMN>

F;60-250/Domain: extracellular #status predicted <EXT>
F;78,156,226,241,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.4%; Score 79; DB 2; Length 250;
Best Local Similarity 26.7%; Pred. No. 0.055;
Matches 12; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY | 4 QNKPPSKPNNDPHEVNFVPCISNNPTCWAICRIPNKKPGK 48
| | | | | : : : : | | | | | : : : : | | : : |
Db | 145 ESNPPHNDHNSQTLFVPCSTCEGNLACLSLCOVGGRAPSR 189

RESULT 15
PQ0769
glycoprotein G - bovine respiratory syncytial virus (isolate VC464) (fragment)
C;Species: bovine respiratory syncytial virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: PQ0769
R;Mallipeddi, S.K.; Samal, S.K.
J. Gen. Virol. 74, 2001-2004, 1993
A;Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial virus
A;Reference number: JQ2284; MUID:93389461; PMID:8376974
A;Accession: PQ0769
A;Molecule type: mRNA
A;Residues: 1-248 <NAL>
A;Experimental source: isolate VC464
A;Note: the authors translated the codon ACC for residue 85 as His and ATC for residue 86
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;1-29/Domain: intracellular #status predicted <INT>
F;30-57/Domain: transmembrane #status predicted <TMN>
F;58-248/Domain: extracellular #status predicted <EXT>
F;76,154,224,242/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.9%; Score 77.5; DB 2; Length 248;
Best Local Similarity 30.8%; Pred. No. 0.081;
Matches 16; Conservative 8; Mismatches 19; Indels 9; Gaps 2;

QY | 6 KPSPKPNNDP-----NNDFFH--FEVNFVPCISNNPTCWAICRIPNKKPGK 48
| | | | | : : : : | | | | | : : : : | | : : |
Db | 136 KPINSGSNPPHNDHNSQTLFVPCSTCEGNLACLSLCOIGPERAPSR 187

Search completed: November 22, 2002, 14:26:59
Job time : 19 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 22, 2002, 14:17:16 ; Search time 11 Seconds
(without alignments)
184.758 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KQRNKPSPKPNDFHFEV.....NNPTCWAICKRIPNKPGRKK 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	288	100.0	298	1 VGLG_HRSVA	P03423 human respi
2	285	99.0	297	1 VGLG_HRSV2	P27021 human respi
3	285	99.0	297	1 VGLG_HRSV3	P27022 human respi
4	285	99.0	297	1 VGLG_HRSV6	P27025 human respi
5	285	99.0	298	1 VGLG_HRSVL	P20895 human respi
6	280	97.2	298	1 VGLG_HRSV5	P27024 human respi
7	279	96.9	297	1 VGLG_HRSV4	P27023 human respi
8	273	94.8	297	1 VGLG_HRSV7	P27026 human respi
9	190	66.0	292	1 VGLG_HRSV1	P20896 human respi
10	190	66.0	292	1 VGLG_HRSV8	P23041 human respi
11	83.5	29.0	257	1 VGLG_BRSCV	P22261 bovine resp
12	80	27.8	263	1 VGLG_BRSV2	O10683 bovine resp
13	77.5	26.9	257	1 VGLG_BRSVS	O10685 bovine resp
14	77.5	26.9	263	1 VGLG_BRSVW	O10687 bovine resp
15	77.5	26.9	263	1 VGLG_ORSVW	O86695 ovine respi
16	76.5	26.6	263	1 VGLG_BRSV1	O10683 bovine resp
17	76.5	26.6	263	1 VGLG_BRSV4	O10684 bovine resp
18	74	25.7	257	1 VGLG_BRSVL	O09495 bovine resp
19	74	25.7	257	1 VGLG_BRSVR	Q84183 bovine resp
20	73	25.3	257	1 VGLG_BRSV7	Q5706 bovine resp
21	67.5	23.4	274	1 DAPF_PASMU	P57962 pasteurella
22	66.5	23.1	274	1 DAPF_ECO57	Q8x8p8 escherichia
23	66.5	23.1	274	1 DAPF_ECOLI	P08885 escherichia
24	66.5	23.1	274	1 DAPF_SALTY	Q91696 salmonella
25	66.5	23.1	274	1 DAPF_YERPE	P46357 yersinia pe
26	64	22.2	37	1 SCK2_LEIQH	P45628 leirus qui
27	63.5	22.0	274	1 DAPF_HAEIN	P44859 haemophilus
28	62	21.5	37	1 SCKC_LEIQH	P13487 leirus qui
29	62	21.5	276	1 DAPF_VIBCH	Q9kvl6 vibrio chol
30	60.5	21.0	57	1 SCKL_MESMA	Q9nll6 mesobuthus
31	58.5	20.3	276	1 DAPF_PSEAE	Q51564 pseudomonas
32	57.5	20.0	276	1 DAPF_PSEFL	O05322 pseudomonas
33	57	19.8	279	1 DAPF_AQUAE	O67693 aquifex aeo

RESULT 1

ID	VGLG_HRSVA	STANDARD;	PRT;	298 AA.
AC	P03423;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	13-JUL-1998 (Rel. 36, Last annotation update)			
DE	Major surface glycoprotein G (Attachment glycoprotein G).			
GN	G.			
OS	Human respiratory syncytial virus (strain A2).			
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;			
OC	Paramyxoviridae; Pneumovirinae; Pneumovirus.			
OX	NCBI_TaxID=11259;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85216636; PubMed=3858865;			
RA	Wertz G.W., Collins P.L., Huang Y., Gruber C., Levine S., Ball L.A.;			
RT	"Nucleotide sequence of the G protein gene of human respiratory			
RT	syncytial virus reveals an unusual type of viral membrane protein.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:4075-4079(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86067198; PubMed=4069997;			
RA	Satake M., Coligan J.E., Elango N., Norby E., Venkatesan S.;			
RT	"Respiratory syncytial virus envelope glycoprotein (G) has a novel			
RT	structure.";			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95266253; PubMed=7747420;			
RA	Connors M., Crowe J.E. Jr., Firestone C.Y., Murphy B.R., Collins P.L.;			
RT	"A cold-passaged, attenuated strain of human respiratory syncytial			
RT	virus contains mutations in the F and L genes.";			
RL	Virology 208:478-484(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97187925; PubMed=9035372;			
RA	Crowe J.E. Jr., Firestone C.Y., Whitehead S.S., Collins P.L.,			
RA	Murphy B.R.;			
RT	"Acquisition of the ts phenotype by a chemically-mutagenized cold-			
RT	passaged human respiratory syncytial virus vaccine candidate results			
RT	from the acquisition of a single mutation in the polymerase (L)			
RT	gene.";			
RL	Virus Genes 13:269-273(1996).			
CC	-1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE			
CC	RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND			
CC	HEMAGGLUTININATING ACTIVITIES.			
CC	-1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED			
CC	CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.			
CC	-1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS			
CC	DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			

ALIGNMENTS

34	56.5	19.6	748	1	JSB1_TRINI	Q06342 trichoplusi
35	55.5	19.3	747	1	SSP1_BOMBO	P09179 bombyx mori
36	55	19.1	35	1	SCKK_TITSE	P56219 tityus serr
37	54.5	18.9	58	1	SCK2_MESMA	Q9nll5 mesobuthus
38	54.5	18.9	902	1	SYGL_YEAST	P40528 saccharomyc
39	54.5	18.9	1067	1	HGBB_HAEIN	Q9kvl1 haemophilus
40	54	18.8	160	1	LSPA_BUCAI	P57248 buchnera ap
41	53.5	18.6	237	1	HK31_MOUSE	P97436 mus musculu
42	52.5	18.2	284	1	DAPF_BUCAI	P57649 buchnera ap
43	52.5	18.2	360	1	MTSB_LACLC	P34878 lactococcus
44	52	18.1	102	1	VE7_PAPVE	P11332 european el
45	52	18.1	454	1	TRIA_MOUSE	P25118 mus musculu

CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).

DR EMBL; M11486; AAB59857.1; -
DR EMBL; X03149; CAA26928.1; -
DR EMBL; U50362; AAB86663.1; -
DR EMBL; U50363; AAB86675.1; -
DR EMBL; U63644; AAC55969.1; -
DR PIR; A04039; MGNZ.
DR InterPro: IPR000925; Glycoprot.G.
DR Pfam: PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein. CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 37
FT TRANSMEM 38 66
FT DOMAIN 67 297
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 298 AA; 32586 MW; 993C3D2DD68BC634 CRC64;

Query Match 100.0%; Score 288; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 6.9e-27;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 49
|||||
DB 149 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 197
|||||

RESULT 2

VGLG_HRSV2
ID VGLG_HRSV2 STANDARD; PRT; 297 AA.
AC P27021;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN G.
OS Human respiratory syncytial virus (strain rsb642).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11252;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374005; PubMed=1895054;
RA Cane P.A., Matthews D.A., Pringle C.R.;
RT "Identification of variable domains of the attachment (G) protein of
RT subgroup A respiratory syncytial viruses.";
RL J. Gen. Virol. 72:2091-2096(1991).
CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC HEMAGGLUTININATING ACTIVITIES.
CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
DR PIR; JQ1204; JQ1204.
DR InterPro: IPR000925; Glycoprot.G.
DR Pfam: PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37
FT TRANSMEM 38 66
FT DOMAIN 67 297
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 297 AA; 32745 MW; FC72A7F3A8BF67C CRC64;

Query Match 99.0%; Score 285; DB 1; Length 297;
Best Local Similarity 98.0%; Pred. No. 1.5e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 49
|||||
DB 149 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKR 197
|||||

RESULT 3

VGLG_HRSV3
ID VGLG_HRSV3 STANDARD; PRT; 297 AA.
AC P27022;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN G.
OS Human respiratory syncytial virus (strain rsb1734).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11253;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374005; PubMed=1895054;
RA Cane P.A., Matthews D.A., Pringle C.R.;
RT "Identification of variable domains of the attachment (G) protein of
RT subgroup A respiratory syncytial viruses.";
RL J. Gen. Virol. 72:2091-2096(1991).
CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC HEMAGGLUTININATING ACTIVITIES.
CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
DR PIR; JQ1205; JQ1205.
DR InterPro: IPR000925; Glycoprot.G.
DR Pfam: PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37
FT TRANSMEM 38 66
FT DOMAIN 67 297
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 297 AA; 32525 MW; 48448F9E091E1802 CRC64;

Query Match 99.0%; Score 285; DB 1; Length 297;
Best Local Similarity 98.0%; Pred. No. 1.5e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 49
|||||
DB 149 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKR 197
|||||

RESULT 4

VGLG_HRSV6
ID VGLG_HRSV6 STANDARD; PRT; 297 AA.
AC P27025;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN G.
OS Human respiratory syncytial virus (strain rsb6256).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11256;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374005; PubMed=1895054;
RA Cane P.A., Matthews D.A., Pringle C.R.;
RT "Identification of variable domains of the attachment (G) protein of
RT subgroup A respiratory syncytial viruses.";
RL J. Gen. Virol. 72:2091-2096(1991).

FT	TRANSMEM	38	66	POTENTIAL.
FT	DOMAIN	67	298	EXTRACELLULAR (POTENTIAL).
FT	CARBOHYD	103	103	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	135	135	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	237	237	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	250	250	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	251	251	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	294	294	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	298 AA;	32781 MW;	B79FEFA4B4A73BOE CRC64;
Query Match				
Best Local Similarity 99.0%; Score 285; DB 1; Length 298;				
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
QY	1	KQRQKPPSPKPNDFHFEVFNFPVPCSSNNPTCWAICKRIPNKKPKKK	49	
Db	149	KQRQKPPKPNDFHFEVFNFPVPCSSNNPTCWAICKRIPNKKPKKK	197	
RESULT 6				
ID	VGLG_HRSV5	STANDARD;	PRT;	298 AA.
AC	P27024;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Major surface glycoprotein G (Attachment glycoprotein G).			
GN	G.			
OS	Human respiratory syncytial virus (strain rsb6190)...			
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;			
OC	Paramyxoviridae; Pneumovirinae; Pneumovirus.			
OX	NCBI_TaxID=11235;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91374005; PubMed=1895054;			
RA	Cane P.A., Matthews D.A., Pringle C.R.;			
RA	"Identification of variable domains of the attachment (G) protein of			
RL	subgroup A respiratory syncytial viruses.";			
RL	J. Gen. Virol. 72:2091-2096(1991).			
CC	-1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE			
CC	RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND			
CC	HEMAGGLUTININATING ACTIVITIES			
CC	-1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED			
CC	CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.			
CC	-1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS			
CC	DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.			
DR	PIR; JQ1207; JQ1207.			
DR	InterPro: IPR000925; Glycoprot_G.			
DR	Pfam: PF00802; Glycoprotein_G; 1.			
KW	Transmembrane; Glycoprotein.			
FT	DOMAIN	1	37	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	38	66	POTENTIAL.
FT	DOMAIN	67	298	EXTRACELLULAR (POTENTIAL).
FT	CARBOHYD	103	103	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	135	135	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	237	237	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	250	250	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	294	294	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	298 AA;	32769 MW;	4D74E854D34D7BA5 CRC64;
Query Match				
Best Local Similarity 97.2%; Score 280; DB 1; Length 298;				
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;				
QY	1	KQRQKPPSPKPNDFHFEVFNFPVPCSSNNPTCWAICKRIPNKKPKKK	49	
Db	149	KQRQKPPKPNDFHFEVFNFPVPCSSNNPTCWAICKRIPNKKPKKK	197	
RESULT 7				
VGLG_HRSV4	STANDARD;	PRT;	297 AA.	
AC	P27023;			

DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN G.
OS Human respiratory syncytial virus (strain rsb5857).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11254;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374005; PubMed=1895054;
RA Cane P.A., Matthews D.A., Pringle C.R.;
RT "Identification of variable domains of the attachment (G) protein of subgroup A respiratory syncytial viruses.";
RL J. Gen. Virol. 72:2091-2096(1991).
CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTININATING ACTIVITIES.
CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
DR PIR; JQ1206; JQ1206.
DR InterPro; IPR000925; Glycoprot_G.
DR Pfam; PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 297 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 297 AA; 32772 MW; 10488CCA475936BE CRC64;
Query Match 96.9%; Score 279; DB 1; Length 297;
Best Local Similarity 95.9%; Pred. No. 7.8e-26;
Matches 47; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KQKQKPPKPNNDHFEVFNPCISCSNNPTCWAICKRIPNKPCKK 49
DB 149 KQKQKPPKPNNDHFEVFNPCISCSNNPTCWAICKRIPNKPCKK 197
RESULT 8
VGLG_HRSV7
ID VGLG_HRSV7 STANDARD; PRT; 297 AA.
AC P27026;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN G.
OS Human respiratory syncytial virus (strain rsb6614).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11257;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374005; PubMed=1895054;
RA Cane P.A., Matthews D.A., Pringle C.R.;
RT "Identification of variable domains of the attachment (G) protein of subgroup A respiratory syncytial viruses.";
RL J. Gen. Virol. 72:2091-2096(1991).
CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTININATING ACTIVITIES.
CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS

CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
DR PIR; JQ1209; JQ1209.
DR InterPro; IPR000925; Glycoprot_G.
DR Pfam; PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 297 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 297 AA; 32670 MW; 58B384028E437ACD CRC64;
Query Match 94.8%; Score 273; DB 1; Length 297;
Best Local Similarity 93.9%; Pred. No. 4e-25;
Matches 46; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 KQKQKPPKPNNDHFEVFNPCISCSNNPTCWAICKRIPNKPCKK 49
DB 149 KQKQKPPKPNNDHFEVFNPCISCSNNPTCWAICKRIPNKPCKK 197
RESULT 9
VGLG_HRSV1
ID VGLG_HRSV1 STANDARD; PRT; 292 AA.
AC P20896;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN G.
OS Human respiratory syncytial virus (subgroup B / strain 18537).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11251;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87289657; PubMed=2441388;
RA Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;
RT "The G glycoprotein of human respiratory syncytial viruses of subgroups A and B: extensive sequence divergence between antigenically related proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).
CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTININATING ACTIVITIES.
CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
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CC -----
DR EMBL; M17213; AAA47412.1; -.
DR PIR; B32703; MGNZ18.
DR InterPro; IPR000925; Glycoprot_G.
DR Pfam; PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 292 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 292 AA; 32306 MW; BC8C59F69CA7AFC2 CRC64;


```
QY | 6 KPSPKPNDF-----HFEVNFVPCISCSNNPTCWAIC-----KRIPNKKP 46
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db | 145 KPPINPSGPPENHQDHNHNSQTLPPVPCSTCEGNLACLCLSLCHLETERAPSR 198
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 12
VGLG_BRSV2
ID VGLG_BRSV2 STANDARD; PRT; 263 AA.
AC O10685;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN Bovine respiratory syncytial virus (strain 220-60) (BRS).
OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=82819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97288324; PubMed=9143302;
RA Furze J., Roberts S., Wertz G., Taylor G.;
RT "Antigenically distinct G glycoproteins of BRSV strains share a high
degree of genetic homogeneity.";
RL Virology 231:48-58(1997).
CC -|- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTININATING ACTIVITIES.
CC -|- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -|- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
HRS VIRUS.
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or send an email to license@isb-sib.ch).
CC
CC EMBL; Y11205; CAAT2089.1; -.
DR HSSP; P22261; IBRV.
DR InterPro; IPR000925; Glycoprot_G.
DR Pfam; PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 263 EXTRACELLULAR (POTENTIAL).
FT DISULFID 173 186 BY SIMILARITY.
FT DISULFID 176 182 BY SIMILARITY.
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 263 AA; 28964 MW; A630883D51ED02D5 CRC64;

Query Match 27.8%; Score 80; DB 1; Length 263;
Best Local Similarity 29.8%; Pred. No. 0.017;
Matches 14; Conservative 9; Mismatches 20; Indels 4; Gaps 1;

QY | 4 ONKPPSKPNDFHFEVNFVPCISCSNNPTCWAIC-----KRIPNKKP 46
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db | 152 ESNPPENHQDHNHNSQTLPPVPCSTCEGNPACSLCIGLERAPSR 198
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 13
VGLG_BRSVS
ID VGLG_BRSVS STANDARD; PRT; 257 AA.
AC O10686;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
```

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GN Bovine respiratory syncytial virus (strain Snook) (BRS).
OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=82824;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97288324; PubMed=9143302;
RA Furze J., Roberts S., Wertz G., Taylor G.;
RT "Antigenically distinct G glycoproteins of BRSV strains share a high
degree of genetic homogeneity.";
RL Virology 231:48-58(1997).
CC -|- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTININATING ACTIVITIES.
CC -|- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -|- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
HRS VIRUS.
CC
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CC
CC EMBL; Y08719; CAA65969.1; -.
DR HSSP; P22261; IBRV.
DR InterPro; IPR000925; Glycoprot_G.
DR Pfam; PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 257 EXTRACELLULAR (POTENTIAL).
FT DISULFID 173 186 BY SIMILARITY.
FT DISULFID 176 182 BY SIMILARITY.
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 257 AA; 28362 MW; 09BDE6874421E79B CRC64;

Query Match 26.9%; Score 77.5; DB 1; Length 257;
Best Local Similarity 30.8%; Pred. No. 0.032;
Matches 16; Conservative 8; Mismatches 19; Indels 9; Gaps 2;

QY | 6 KPSPKP-----NNDFF--FEVNFVPCISCSNNPTCWAICKRIPNKKPKG 48
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db | 145 KPPINPSGPPENHQDHNHNSQTLPPVPCSTCEGNLACLCLCIGPERAPSR 196
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 14
VGLG_BRSVM
ID VGLG_BRSVM STANDARD; PRT; 263 AA.
AC O10687;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN Bovine respiratory syncytial virus (strain Wbh) (BRS).
OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=82825;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97288324; PubMed=9143302;
RA Furze J., Roberts S., Wertz G., Taylor G.;
RT "Antigenically distinct G glycoproteins of BRSV strains share a high
degree of genetic homogeneity.";
RL Virology 231:48-58(1997).
```

CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC HEMAGGLUTININATING ACTIVITIES.
CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
CC HRS VIRUS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y08717; CAA69967.1; -.
DR HSP; P22261; IBRV.
DR InterPro; IPR000925; Glycoprot_G.
DR Pfam; PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 263 EXTRACELLULAR (POTENTIAL).
FT DISULFID 173 186 BY SIMILARITY.
FT CARBOHYD 176 182 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 263 AA; 29050 MW; 0D06AF7FCB46B858 CRC64;
Query Match 26.9%; Score 77.5; DB 1; Length 263;
Best Local Similarity 29.0%; Pred. No. 0.033;
Matches 20; Conservative 5; Mismatches 19; Indels 25; Gaps 3;
Qy 6 KPPSKP-----NNDFH--FEVFNFPVCSICSNPTCWAIC-----KR 40
Db 145 KPPINPSSNPENHQNNSQTLPHVPCSTCEGNCACSLICQIGPERASSRAPITLKK 204
Qy 41 IPNKKPKKK 49
Db 205 TPKPTTKK 213
RESULT 15
VGLG_ORSVW
ID VGLG_ORSVW STANDARD; PRT; 263 AA.
AC Q86695;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN G.
OS Ovine respiratory syncytial virus (strain WSU 83-1578) (ORSV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=79699;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94103788; PubMed=8277288;
RA Mallipeddi S.K.; Samal S.K.;
RT "Analysis of the ovine respiratory syncytial virus (RSV) G
RT glycoprotein gene defines a subgroup of ungulate RSV.";
RL J. Gen. Virol. 74:2787-2791(1993).
CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC HEMAGGLUTININATING ACTIVITIES.
CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
CC HRS VIRUS.
CC -----

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CC -----
DR EMBL; S67863; AAB29551.1; -.
DR EMBL; S67862; AAB29551.1; JOINED.
DR HSP; P22261; IBRV.
DR InterPro; IPR000925; Glycoprot_G.
DR Pfam; PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 263 EXTRACELLULAR (POTENTIAL).
FT DISULFID 173 186 BY SIMILARITY.
FT CARBOHYD 176 182 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 263 AA; 29225 MW; 81A649C6047B3B71 CRC64;
Query Match 26.9%; Score 77.5; DB 1; Length 263;
Best Local Similarity 25.8%; Pred. No. 0.033;
Matches 17; Conservative 10; Mismatches 18; Indels 21; Gaps 2;
Qy 4 QNKPPSPNDF--HFEVFNFPVCSICSNPTCWAIC-----KRIP 42
Db 151 QKSNPSETQDYSDFIQLPYVPCNICEGDSACLSLCQDRSESLDKALTTTPKTKPKPMT 210
Qy 43 NKKPKG 48
Db 211 TKKPTK 216
Search completed: November 22, 2002, 14:25:58
Job time : 12 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 22, 2002, 14:24:12 ; Search time 29 Seconds
(without alignments)
348.149 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KORQKPPSKPNDHFHFV.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	DB ID	Description
1	288	100.0	293	12	Q9YVB3 human respi
2	285	99.0	278	12	Q9Q6U1 human respi
3	285	99.0	278	12	Q9Q6T7 human respi
4	285	99.0	278	12	Q9Q6T4 human respi
5	285	99.0	278	12	Q9Q6T3 human respi
6	285	99.0	278	12	Q9Q6T0 human respi
7	285	99.0	279	12	Q9Q6U0 human respi
8	285	99.0	279	12	Q9Q6T9 human respi
9	285	99.0	279	12	Q9Q6T8 human respi
10	285	99.0	279	12	Q9Q6T5 human respi
11	285	99.0	279	12	Q9Q6T2 human respi
12	285	99.0	279	12	Q9Q6S9 human respi
13	285	99.0	279	12	Q9Q6S7 human respi
14	285	99.0	279	12	Q9Q6S6 human respi
15	285	99.0	279	12	Q9Q6S0 human respi
16	285	99.0	279	12	Q9Q6R9 human respi

17	285	99.0	292	12	Q9YVB2	Q9YVB2 human respi
18	285	99.0	292	12	Q9YVB0	Q9YVB0 human respi
19	285	99.0	295	12	Q86356	Q86356 respiratory
20	285	99.0	295	12	Q86359	Q86359 respiratory
21	285	99.0	295	12	Q86360	Q86360 respiratory
22	285	99.0	297	12	Q82074	Q82074 human respi
23	285	99.0	297	12	Q82078	Q82078 human respi
24	285	99.0	297	12	Q82066	Q82066 human respi
25	285	99.0	297	12	Q82067	Q82067 human respi
26	285	99.0	297	12	Q82071	Q82071 human respi
27	285	99.0	297	12	Q82057	Q82057 human respi
28	285	99.0	297	12	Q82058	Q82058 human respi
29	285	99.0	297	12	Q9YVB5	Q9YVB5 human respi
30	285	99.0	298	12	Q82073	Q82073 human respi
31	285	99.0	298	12	Q82065	Q82065 human respi
32	285	99.0	298	12	Q82068	Q82068 human respi
33	285	99.0	298	12	Q82075	Q82075 respiratory
34	285	99.0	298	12	Q09634	Q09634 human respi
35	285	99.0	298	12	Q01929	Q01929 human respi
36	285	97.2	279	12	Q9Q6S8	Q9Q6S8 human respi
37	280	97.2	293	12	Q9YVB1	Q9YVB1 human respi
38	280	97.2	296	12	Q86358	Q86358 respiratory
39	280	97.2	297	12	Q91944	Q91944 human respi
40	280	97.2	298	12	Q82061	Q82061 human respi
41	280	97.2	298	12	Q82075	Q82075 human respi
42	280	97.2	298	12	Q82076	Q82076 human respi
43	280	97.2	298	12	Q82062	Q82062 human respi
44	280	97.2	298	12	Q82056	Q82056 human respi
45	280	97.2	298	12	Q82060	Q82060 human respi

ALIGNMENTS

RESULT 1

Q9YVB3 ID Q9YVB3 PRELIMINARY; PRT; 293 AA.
AC Q9YVB3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Attachment glycoprotein G (Fragment).
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_taxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VV6973;
RX MEDLINE=99022964; PubMed=9806017;
RA Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
RT "Antigenic and genetic diversity among the attachment proteins of
RT group A respiratory syncytial viruses that have caused repeat
RT infections in children."
RL J. Infect. Dis. 178:925-932(1998).
DR EMBL; AF065407; AAD02943.1; -
DR InterPro; IPR000925; Glycoprot G.
DR InterPro; IPR003880; Ppantne.attach.
DR InterPro; IPR002965; P_rich_extensn.
DR Pfam; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 293 AA; 32125 MW; 17B5B43396A63CCF CRC64;

Query Match 100.0%; Score 288; DB 12; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.6e-31;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KORQKPPSKPNDHFHFVFPVCSICSNPTCWAICKRIPNKKPGKK 49
Db 144 KORQKPPSKPNDHFHFVFPVCSICSNPTCWAICKRIPNKKPGKK 192


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DR EMBL: AF193313; AAF23736.1; -
DR InterPro: IPR000925; Glycoprot.G.
DR InterPro: IPR003880; Ppantne.attach.
DR Pfam: PF00802; Glycoprotein_G; 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30443 MW; 8E2974F2E1AE15C9 CRC64;

Query Match 99.0%; Score 285; DB 12; Length 278;
Best Local Similarity 98.0%; Pred. No. 3.8e-31;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORONKPPSKPNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 130 KORQKPPNKNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 178

RESULT 6
Q906T0 PRELIMINARY; PRT; 278 AA.
AC Q906T0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Glycoprotein (Fragment).
DE Glycoprotein_G; 1.
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=94191.
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroups A and B of respiratory syncytial virus isolated over 9
RT consecutive epidemics in Korea.";
RL J. Infect. Dis. 181:1547-1556(2000).
DR EMBL: AF193316; AAF23739.1; -
DR InterPro: IPR000925; Glycoprot.G.
DR InterPro: IPR003880; Ppantne.attach.
DR Pfam: PF00802; Glycoprotein_G; 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30440 MW; 8D38997DEB9A6292 CRC64;

Query Match 99.0%; Score 285; DB 12; Length 278;
Best Local Similarity 98.0%; Pred. No. 3.8e-31;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORONKPPSKPNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 49
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Db 130 KORQKPPNKNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 178

RESULT 7
Q906U0 PRELIMINARY; PRT; 279 AA.
AC Q906U0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Glycoprotein (Fragment).
DE Glycoprotein_G; 1.
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
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RN SEQUENCE FROM N.A.
RP STRAIN=91242;
RX MEDLINE=20283719; PubMed=10823752;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroups A and B of respiratory syncytial virus isolated over 9
RT consecutive epidemics in Korea.";
RL J. Infect. Dis. 181:1547-1556(2000).
DR EMBL: AF193306; AAF23729.1; -
DR InterPro: IPR000925; Glycoprot.G.
DR InterPro: IPR003880; Ppantne.attach.
DR Pfam: PF00802; Glycoprotein_G; 1.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30544 MW; 6B270AAEB1CB3533 CRC64;

Query Match 99.0%; Score 285; DB 12; Length 279;
Best Local Similarity 98.0%; Pred. No. 3.8e-31;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORONKPPSKPNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 130 KORQKPPNKNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 178

RESULT 8
Q906T9 PRELIMINARY; PRT; 279 AA.
AC Q906T9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Glycoprotein (Fragment).
DE Glycoprotein_G; 1.
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=91399;
RX MEDLINE=20283719; PubMed=10823752;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroups A and B of respiratory syncytial virus isolated over 9
RT consecutive epidemics in Korea.";
RL J. Infect. Dis. 181:1547-1556(2000).
DR EMBL: AF193307; AAF23730.1; -
DR InterPro: IPR000925; Glycoprot.G.
DR InterPro: IPR003880; Ppantne.attach.
DR Pfam: PF00802; Glycoprotein_G; 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30570 MW; AF6CF9C1D8F8A97C CRC64;

Query Match 99.0%; Score 285; DB 12; Length 279;
Best Local Similarity 98.0%; Pred. No. 3.8e-31;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORONKPPSKPNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 130 KORQKPPNKNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 178

RESULT 9
Q906T8 PRELIMINARY; PRT; 279 AA.
AC Q906T8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Glycoprotein (Fragment).
GN G.

OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=92011;
RX MEDLINE=20283719; PubMed=10823752;

RA Choi E.H., Lee H.J.;

RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroups A and B of respiratory syncytial virus isolated over 9
RT consecutive epidemics in Korea.";

RL J. Infect. Dis. 181:1547-1556(2000).

DR EMBL; AF193308; AAF23731.1; -

DR InterPro; IPR000925; Glycoprot_G.

DR InterPro; IPR003880; Ppantne_attach.

DR Pfam; PF00802; Glycoprotein_G; 1.

DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.

FT NON_TER 1

SQ SEQUENCE 279 AA; 30498 MW; 4E1CDF2F7E569E3A CRC64;

Query Match 99.0%; Score 285; DB 12; Length 279;
Best Local Similarity 98.0%; Pred. No. 3.8e-31;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPKPNDFHFVFNPCISNNPTCWAICKRIPNKKPGKK 49

DB 130 KORQKPPKPNDFHFVFNPCISNNPTCWAICKRIPNKKPGKK 178

- RESULT 10

Q906T5

ID Q906T5 PRELIMINARY; PRT; 279 AA.

AC Q906T5;

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)

DE Glycoprotein (Fragment).

GN G.

OS Human respiratory syncytial virus.

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Pneumovirinae; Pneumovirus.

OX NCBI_TaxID=11250;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=92415;
RX MEDLINE=20283719; PubMed=10823752;

RA Choi E.H., Lee H.J.;

RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroups A and B of respiratory syncytial virus isolated over 9
RT consecutive epidemics in Korea.";

RL J. Infect. Dis. 181:1547-1556(2000).

DR EMBL; AF193311; AAF23734.1; -

DR InterPro; IPR000925; Glycoprot_G.

DR InterPro; IPR003880; Ppantne_attach.

DR InterPro; IPR002965; P_rich_extensn.

DR Pfam; PF00802; Glycoprotein_G; 1.

DR PRINTS; PR01217; PRICHEXTNSN.

DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.

FT NON_TER 1

SQ SEQUENCE 279 AA; 30442 MW; F53F5932FCE77E89 CRC64;

Query Match 99.0%; Score 285; DB 12; Length 279;
Best Local Similarity 98.0%; Pred. No. 3.8e-31;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPKPNDFHFVFNPCISNNPTCWAICKRIPNKKPGKK 49

DB 130 KORQKPPKPNDFHFVFNPCISNNPTCWAICKRIPNKKPGKK 178

RESULT 11

Q906T2

ID Q906T2 PRELIMINARY; PRT; 279 AA.

AC Q906T2;

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)

DE Glycoprotein (Fragment).

GN G.

OS Human respiratory syncytial virus.

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Pneumovirinae; Pneumovirus.

OX NCBI_TaxID=11250;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=93057;
RX MEDLINE=20283719; PubMed=10823752;

RA Choi E.H., Lee H.J.;

RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroups A and B of respiratory syncytial virus isolated over 9
RT consecutive epidemics in Korea.";

RL J. Infect. Dis. 181:1547-1556(2000).

DR EMBL; AF193314; AAF23737.1; -

DR InterPro; IPR000925; Glycoprot_G.

DR InterPro; IPR003880; Ppantne_attach.

DR InterPro; IPR002965; P_rich_extensn.

DR Pfam; PF00802; Glycoprotein_G; 1.

DR PRINTS; PR01217; PRICHEXTNSN.

DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.

FT NON_TER 1

SQ SEQUENCE 279 AA; 30547 MW; 86DFD42DC8A8F500 CRC64;

Query Match 99.0%; Score 285; DB 12; Length 279;
Best Local Similarity 98.0%; Pred. No. 3.8e-31;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 130 KORQKPPKPNDFHFVFNPCISNNPTCWAICKRIPNKKPGKK 178

RESULT 12

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ID Q906S9 PRELIMINARY; PRT; 279 AA.

AC Q906S9;

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)

DE Glycoprotein (Fragment).

GN G.

OS Human respiratory syncytial virus.

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Pneumovirinae; Pneumovirus.

OX NCBI_TaxID=11250;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=95026;
RX MEDLINE=20283719; PubMed=10823752;

RA Choi E.H., Lee H.J.;

RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroups A and B of respiratory syncytial virus isolated over 9
RT consecutive epidemics in Korea.";

RL J. Infect. Dis. 181:1547-1556(2000).

DR EMBL; AF193317; AAF23740.1; -

DR InterPro; IPR000925; Glycoprot_G.

DR InterPro; IPR003880; Ppantne_attach.

DR InterPro; IPR002965; P_rich_extensn.

DR Pfam; PF00802; Glycoprotein_G; 1.

DR PRINTS; PR01217; PRICHEXTNSN.

DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.

FT NON_TER 1

SQ SEQUENCE 279 AA; 30529 MW; AEC4D787983D472D CRC64;

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 22, 2002, 14:26:37 ; Search time 11 Seconds
(without alignments)
69.765 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/ECTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	62	21.5	37	10	US-09-030-619-181
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3	54	18.8	57	9	US-10-044-359-20
4	53	18.4	58	9	US-10-044-359-18
5	51	17.7	36	9	US-10-044-359-27
6	51	17.7	325	9	US-10-033-245-11
7	51	17.7	325	9	US-10-033-223-11
8	51	17.7	325	12	US-10-033-246-11
9	51	17.7	325	12	US-10-033-301-11
10	51	17.7	325	12	US-10-033-326-11
11	50.5	17.5	35	10	US-09-864-761-48887
12	50	17.4	58	9	US-10-044-359-16
13	50	17.4	102	10	US-09-864-761-35081
14	50	17.4	1010	10	US-09-759-152-2
15	50	17.4	1024	10	US-09-879-257A-30
16	49.5	17.2	217	10	US-09-853-161-71
17	49.5	17.2	217	10	US-09-852-659A-71
18	49.5	17.2	322	10	US-09-726-643-72
19	49.5	17.2	453	10	US-09-726-643-46

20	49.5	17.2	489	10	US-09-726-643-82
21	49.5	17.2	489	10	US-09-925-300-1151
22	49.5	17.2	1940	9	US-10-016-283-34
23	49	17.0	74	10	US-09-989-903-18
24	48.5	16.8	185	10	US-09-854-864-11
25	48.5	16.8	271	10	US-09-864-761-37986
26	48.5	16.8	281	10	US-09-854-864-10
27	48.5	16.8	465	9	US-09-987-021-6
28	48.5	16.8	465	10	US-09-957-485-6
29	48.5	16.8	566	10	US-09-801-368-418
30	48	16.7	67	10	US-09-764-887-215
31	48	16.7	461	9	US-09-898-234-15
32	48	16.7	461	9	US-09-899-429A-25
33	48	16.7	461	10	US-09-889-422-15
34	48	16.7	712	10	US-09-888-615-69
35	47.5	16.5	87	10	US-09-764-869-949
36	47.5	16.5	449	10	US-09-801-574-84
37	47.5	16.5	542	10	US-09-908-805B-44
38	47.5	16.5	553	10	US-09-888-224-2
39	47.5	16.5	608	10	US-09-803-589-2
40	47.5	16.5	608	10	US-09-803-589-8
41	47.5	16.5	608	12	US-10-105-929-13
42	47.5	16.5	727	10	US-09-445-023A-1
43	47.5	16.5	835	10	US-09-801-574-22
44	47.5	16.5	967	12	US-10-105-929-2
45	47	16.3	60	10	US-09-864-761-40201

ALIGNMENTS

RESULT 1

US-09-030-619-181

; Sequence 181, Application US/09030619B

; Patent No. US20020035061A1

; GENERAL INFORMATION:

; APPLICANT: Krieger, Timothy J.

; APPLICANT: Taylor, Robert

; APPLICANT: Erfile, Douglas

; APPLICANT: Fraser, Janet R.

; APPLICANT: West, Michael H.P.

; APPLICANT: McNicol, Patricia J.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION

; TITLE OF INVENTION: WITH ANTIBIOTICS

; FILE REFERENCE: 660081.406

; CURRENT APPLICATION NUMBER: US/09/030,619B

; NUMBER OF SEQ ID NOS: 232

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 181

; LENGTH: 37

; TYPE: PRT

; ORGANISM: Leiurus quin-questriatus hebraeus

; US-09-030-619-181

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

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0;

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RESULT 4
US-10-045-359-18
; Sequence 18, Application US/10044359
; Patent No. US20202160454A1
; GENERAL INFORMATION :
; APPLICANT: Hertman, Rafael
; APPLICANT: Wong, James P.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: B#1367 US NA
; CURRENT APPLICATION NUMBER: US/10/0
; CURRENT FILING DATE: 2002-01-11

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RESULT 6
US-10-033-245-11
; Sequence 11, Application US/10033245
; Patent No. US20202160392A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austrey L.
; APPLICANT: Pan, James
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Tr

```

;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2930RIC7
;; CURRENT APPLICATION NUMBER: US/10/033,245
;; CURRENT FILING DATE: 2001-12-27
;; PRIOR APPLICATION NUMBER: 60/095,325
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: 60/112,851
;; PRIOR FILING DATE: 1998-12-16
;; PRIOR APPLICATION NUMBER: 60/113,145
;; PRIOR FILING DATE: 1998-12-16
;; PRIOR APPLICATION NUMBER: 60/113,511
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 60/115,558
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115,565
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115,733
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/119,341
;; PRIOR FILING DATE: 1999-02-09
;; PRIOR APPLICATION NUMBER: 60/119,537
;; PRIOR FILING DATE: 1999-02-10
;; PRIOR APPLICATION NUMBER: 60/119,965
;; PRIOR FILING DATE: 1999-02-12
;; PRIOR APPLICATION NUMBER: 60/162,506
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: 60/170,262
;; PRIOR FILING DATE: 1999-12-09
;; PRIOR APPLICATION NUMBER: 60/187,202
;; PRIOR FILING DATE: 2000-03-03
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28634
;; PRIOR FILING DATE: 1999-12-01
;; PRIOR APPLICATION NUMBER: PCT/US99/28551
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: 2000-02-11
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: 2000-03-02
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: 2000-03-30
;; PRIOR APPLICATION NUMBER: PCT/US00/14941
;; PRIOR FILING DATE: 2000-05-30
;; PRIOR APPLICATION NUMBER: PCT/US00/15264
;; PRIOR FILING DATE: 2000-06-02
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
;; NUMBER OF SEQ ID NOS: 38
;; SEQ ID NO 11
;; LENGTH: 325
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-033-245-11

Query Match 17.7%; Score 51; DB 9; Length 325;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 25 CSICSNPTCWAICKRIP 42
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Db 270 CPICKGNPCFAETAVIP 287

RESULT 7

US-10-033-223-11
; Sequence 11, Application US/10033223
; Patent No. US20020164646A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc

;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Pan, James
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2930RIC9
;; CURRENT APPLICATION NUMBER: US/10/033,223
;; CURRENT FILING DATE: 2001-12-27
;; PRIOR APPLICATION NUMBER: 60/095,325
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: 60/112,851
;; PRIOR FILING DATE: 1998-12-16
;; PRIOR APPLICATION NUMBER: 60/113,145
;; PRIOR FILING DATE: 1998-12-16
;; PRIOR APPLICATION NUMBER: 60/113,511
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 60/115,558
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115,565
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115,733
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/119,341
;; PRIOR FILING DATE: 1999-02-09
;; PRIOR APPLICATION NUMBER: 60/119,537
;; PRIOR FILING DATE: 1999-02-10
;; PRIOR APPLICATION NUMBER: 60/119,965
;; PRIOR FILING DATE: 1999-02-12
;; PRIOR APPLICATION NUMBER: 60/162,506
;; PRIOR FILING DATE: 1999-10-29
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;; PRIOR APPLICATION NUMBER: 60/187,202
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;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28634
;; PRIOR FILING DATE: 1999-12-01
;; PRIOR APPLICATION NUMBER: PCT/US99/28551
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: 2000-02-11
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: 2000-03-02
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: 2000-03-30
;; PRIOR APPLICATION NUMBER: PCT/US00/14941
;; PRIOR FILING DATE: 2000-05-30
;; PRIOR APPLICATION NUMBER: PCT/US00/15264
;; PRIOR FILING DATE: 2000-06-02
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
;; NUMBER OF SEQ ID NOS: 38
;; SEQ ID NO 11
;; LENGTH: 325
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-033-223-11

Query Match 17.7%; Score 51; DB 9; Length 325;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 25 CSICSNPTCWAICKRIP 42
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Db 270 CPICKGNPCFAETAVIP 287

RESULT 8

US-10-033-246-11
; Sequence 11, Application US/10033246
; Patent No. US20020098505A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2930R1C12
; CURRENT APPLICATION NUMBER: US/10/033,246
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: 60/095,325
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/112,851
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113,145
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113,511
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; PRIOR APPLICATION NUMBER: 60/115,558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115,565
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115,733
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; PRIOR APPLICATION NUMBER: 60/119,341
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; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/119,965
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 60/162,506
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; PRIOR APPLICATION NUMBER: 60/170,262
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; PRIOR APPLICATION NUMBER: PCT/US99/28634
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; PRIOR APPLICATION NUMBER: PCT/US99/28551
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; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/14941
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/32678

; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 11
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-246-11

Query Match 17.7%; Score 51; DB 12; Length 325;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 25 CSICSNPTCWAICKRIP 42
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Db 270 CPICKGNPCFAETAVIP 287

RESULT 9

US-10-033-301-11
; Sequence 11, Application US/10033301
; Patent No. US20020098506A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2930R1C6
; CURRENT APPLICATION NUMBER: US/10/033,301
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/095,325
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/112,851
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113,145
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113,511
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/115,558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115,565
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115,733
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119,341
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; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 60/162,506
; PRIOR FILING DATE: 1999-10-29
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; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/187,202
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; PRIOR APPLICATION NUMBER: PCT/US99/28634
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; PRIOR APPLICATION NUMBER: PCT/US99/28551
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; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 11
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-301-11

Query Match 17.7%; Score 51; DB 12; Length 325;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 25 CSICSNPTCWAICKRIP 42
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DB 270 CPICKNGPNCFAETA VIP 287

RESULT 10
US-10-033-326-11
; Sequence 11, Application US/10033326
; Patent No. US20020098507A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2930RIC8
; CURRENT APPLICATION NUMBER: US/10/033.326
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/095,325
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/112,851
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113,145
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113,511
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/115,558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115,565
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115,733
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119,341
; PRIOR FILING DATE: 1999-02-09
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; PRIOR APPLICATION NUMBER: 60/119,965
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; PRIOR APPLICATION NUMBER: 60/162,506

; PRIOR FILING DATE: 1999-10-29
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; PRIOR FILING DATE: 1999-12-09
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; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/US99/12252
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; PRIOR APPLICATION NUMBER: PCT/US99/28634
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; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/14941
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 11
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-326-11

Query Match 17.7%; Score 51; DB 12; Length 325;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 25 CSICSNPTCWAICKRIP 42
| | | | | | | | | |
DB 270 CPICKNGPNCFAETA VIP 287

RESULT 11
US-09-864-761-48887
; Sequence 48887, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

Best Local Similarity 30.0%; Pred. No. 15;
Matches 12; Conservative 4; Mismatches 8; Indels 16; Gaps 3;
QY 2 QRKNPPSPNDFHFEVNFVPCSCSNNPTCWAICR 40
DB 60 QNRNPPPR-----PCPLCQGNH--WKVHCPR 84

RESULT 14
US-09-759-152-2
; Sequence 2, Application US/09759152
; Patent No. US20020028433A1
; GENERAL INFORMATION:
; APPLICANT: Palmer, Michelle A.J.
; APPLICANT: Gee, Melissa
; APPLICANT: Tillotson, Bonnie
; APPLICANT: Chang, Xiao-Jia
; TITLE OF INVENTION: Systems for Sensitive Detection of G-Protein Coupled
; TITLE OF INVENTION: Receptor and Orphan Receptor Function Using Reporter
; FILE REFERENCE: 4085-235-27 CIP
; CURRENT APPLICATION NUMBER: US/09/759,152
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 09/654,499
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 60/180,669
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1010
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PICAST ALC.
US-09-759-152-2

Query Match 17.4%; Score 50; DB 10; Length 1010;
Best Local Similarity 38.7%; Pred. No. 1.7e+02;
Matches 12; Conservative 3; Mismatches 10; Indels 6; Gaps 1;
QY 10 KPNDHFHFEVNFVPCSCSNNPTCWAICR 40
DB 350 KONN-----FNAVRCSHYPNHPWLTCLDR 374

RESULT 15
US-09-879-257A-30
; Sequence 30, Application US/09879257A
; Patent No. US20020081690A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, SACHIKO
; APPLICANT: HANADA, TOSHIRO
; APPLICANT: SHIRO, MINORO
; APPLICANT: KOBATAKE, SHINZO
; TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF
; FILE REFERENCE: 55986(70281)
; CURRENT APPLICATION NUMBER: US/09/879,257A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 1024
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-879-257A-30

Query Match 17.4%; Score 50; DB 10; Length 1024;
Best Local Similarity 38.7%; Pred. No. 1.7e+02;
Matches 12; Conservative 3; Mismatches 10; Indels 6; Gaps 1;
QY 10 KPNDHFHFEVNFVPCSCSNNPTCWAICR 40
DB 350 KONN-----FNAVRCSHYPNHPWLTCLDR 374

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OM protein - protein search, using sw model

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(without alignments)
96.115 Million cell updates/sec

Title: US-09-202-035-1
Perfect score: 288
Sequence: 1 KORQKPPSKPNDFFHFEV.....NNPTCWAICKRIPNKKPGKK 49

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Searched: 262574 seqs, 2942292 residues

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Minimum DB seq length: 0
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	288	100.0	681	6	Patent No. 5194595
2	285	99.0	298	2	Sequence 8, Appli
3	285	99.0	298	2	Sequence 8, Appli
4	285	99.0	298	3	Sequence 8, Appli
5	285	99.0	298	3	Sequence 8, Appli
6	285	99.0	298	4	Sequence 8, Appli
7	285	99.0	298	4	Sequence 8, Appli
8	285	99.0	298	4	Sequence 8, Appli
9	217	75.3	37	3	Sequence 12, Appli
10	193	67.0	32	3	Sequence 8, Appli
11	174	60.4	28	3	Sequence 4, Appli
12	151	52.4	37	3	Sequence 11, Appli
13	146	50.7	26	4	Sequence 9, Appli
14	145	50.3	30	4	Sequence 6, Appli
15	138	47.9	32	3	Sequence 7, Appli
16	134	46.5	23	4	Sequence 10, Appli
17	129	44.8	30	4	Sequence 5, Appli
18	125	43.4	28	3	Sequence 3, Appli
19	96	33.3	15	4	Sequence 53, Appli
20	96	33.3	16	3	Sequence 13, Appli
21	80	27.8	263	5	Sequence 13, Appli
22	66	22.9	32	3	Sequence 6, Appli
23	65	22.9	37	3	Sequence 10, Appli
24	65	22.6	28	3	Sequence 2, Appli
25	64	22.2	14	3	Sequence 9, Appli
26	64	22.2	14	4	Sequence 9, Appli
27	64	22.2	14	4	Sequence 9, Appli

28	64	22.2	17	3	US-08-721-979A-20	Sequence 20, Appl
29	64	22.2	17	4	US-08-836-501-20	Sequence 20, Appl
30	64	22.2	17	4	US-09-654-289-20	Sequence 20, Appl
31	64	22.2	28	3	US-08-793-792-1	Sequence 1, Appli
32	64	22.2	32	3	US-08-793-792-5	Sequence 5, Appli
33	64	22.2	37	3	US-08-793-792-9	Sequence 9, Appli
34	61	21.2	17	3	US-08-721-979A-19	Sequence 19, Appl
35	61	21.2	17	4	US-08-836-501-19	Sequence 19, Appl
36	61	21.2	17	4	US-09-654-289-19	Sequence 19, Appl
37	54	18.8	14	3	US-08-721-979A-11	Sequence 11, Appl
38	54	18.8	14	4	US-08-836-501-11	Sequence 11, Appl
39	54	18.8	14	4	US-09-654-289-11	Sequence 11, Appl
40	51	17.7	198	1	US-08-052-681-1	Sequence 1, Appli
41	50.5	17.5	115	2	US-08-540-406-8	Sequence 8, Appli
42	50.5	17.5	115	3	US-08-656-055-8	Sequence 8, Appli
43	50.5	17.5	115	4	US-08-954-668-8	Sequence 8, Appli
44	50.5	17.5	115	4	US-08-918-658-8	Sequence 8, Appli
45	50.5	17.5	115	5	PCT-US95-13233-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
5194595-19
; Patent No. 5194595
; APPLICANT: WATHEN, MICHAEL W.
; TITLE OF INVENTION: CHIMERIC GLYCOPROTEINS CONTAINING
; IMMUNOGENIC SEGMENT OF THE GLYCOPROTEINS OF HUMAN RESPIRATORY
; SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/543,780
; FILING DATE: 31-OCT-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 137,387
; FILING DATE: 23-DEC-1987
; SEQ ID NO:19:
; LENGTH: 681
5194595-19

Query Match 100.0%; Score 288; DB 6; Length 681;
Best Local Similarity 100.0%; Pred. No. 1.7e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFFHFEVFNPCISCSNNPTCWAICKRIPNKKPGKK 49
DB 543 KORQKPPSKPNDFFHFEVFNPCISCSNNPTCWAICKRIPNKKPGKK 591

RESULT 2

US-08-467-963C-8
; Sequence 8, Application US/08467963C
; Patent No. 5968776
; GENERAL INFORMATION:
; APPLICANT: KLEIN, Michel H
; APPLICANT: DU, Run-Pan
; APPLICANT: EWASYSHYN, Mary E
; TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

00/0007 NO. 14289


```

; TITLE OF INVENTION: Antigenic peptides derived from the
; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis
; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
; NUMBER OF SEQUENCES: 13

```

Query Match	50.7%	Score 146;	DB 4;	Length 26;
Best Local Similarity	100.0%	Pred. No. 4.4e-11;		

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 22, 2002, 14:16:41 ; Search time 35 seconds
(without alignments)
186.551 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KQRNKPSPKPNDFHFEV.....NNPTCAICKRIPNKKPGKK 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	288	100.0	49	AAW39217	Human RSV A subtyp
2	288	100.0	49	AAW39244	Human RSV G protei
3	288	100.0	49	AAW39248	Human RSV G protei
4	288	100.0	49	AAW39250	Human RSV G protei
5	288	100.0	49	AAW39251	Human RSV G protei
6	288	100.0	298	8 AAP70845	Sequence of human
7	288	100.0	298	13 AAR25302	HSRV glycoprotein
8	288	100.0	298	19 AAW47605	HRSV glycoprotein
9	288	100.0	298	23 AAU74676	Respiratory syncyt
10	288	100.0	681	10 AAP90441	Chimeric human res

11	285	99.0	49	19 AAW39218	Human RSV A subtyp
12	285	99.0	49	19 AAW39219	Human RSV A subtyp
13	285	99.0	49	19 AAW39221	Human RSV A subtyp
14	285	99.0	49	19 AAW39222	Human RSV A subtyp
15	285	99.0	49	19 AAW39223	Human RSV A subtyp
16	285	99.0	49	19 AAW39224	Human RSV A subtyp
17	285	99.0	59	17 AAR97073	Respiratory Syncyt
18	285	99.0	59	20 AAY44100	RSV G protein anti
19	285	99.0	59	22 AAB84145	Amino acid sequenc
20	285	99.0	61	17 AAR97072	Respiratory Syncyt
21	285	99.0	61	20 AAY44099	RSV G protein anti
22	285	99.0	61	22 AAB84144	Amino acid sequenc
23	285	99.0	101	16 AAR88253	RSV subgroup A wi
24	285	99.0	101	17 AAR95610	RSV sub-group A wi
25	285	99.0	101	17 AAR95616	Respiratory Syncyt
26	285	99.0	101	17 AAR97050	RSV G protein anti
27	285	99.0	101	20 AAY44078	A G2Na peptide der
28	285	99.0	101	21 AAB18805	Amino acid sequenc
29	285	99.0	101	22 AAG67741	Amino acid sequenc
30	285	99.0	101	22 AAB84123	Amino acid sequenc
31	285	99.0	101	22 AAB68016	Amino acid sequenc
32	285	99.0	101	22 AAB67775	Amino acid sequenc
33	285	99.0	232	20 AAR96314	Secreted G protein
34	285	99.0	298	14 AAR39286	Respiratory syncyt
35	285	99.0	298	20 AAR96313	Membrane bound G p
36	285	99.0	349	17 AAR95660	Streptococcal prot
37	285	99.0	349	22 AAB68028	Amino acid sequenc
38	285	99.0	452	22 AAB67771	Amino acid sequenc
39	283	98.3	49	19 AAW39220	Human RSV A subtyp
40	280	97.2	57	17 AAR97074	Respiratory Syncyt
41	280	97.2	57	20 AAY44101	RSV G protein anti
42	280	97.2	57	22 AAB84146	Amino acid sequenc
43	270	93.8	101	20 AAR97311	Peptide which indu
44	269	93.4	55	17 AAR97075	Respiratory Syncyt
45	269	93.4	55	20 AAY44102	RSV G protein anti

ALIGNMENTS

RESULT 1

AAW39217
ID AAW39217 standard; peptide: 49 AA.

XX AAW39217;

XX 27-AUG-1998 (first entry)

XX Human RSV A subtype G protein fragment (aa. 149-157) strain A2.

XX G protein; treatment; prevention; diagnosis; infection; immunity; antibody; Pneumovirus; identification; vaccine; cell receptor.

XX Human respiratory syncytial virus.

XX Key Location/Qualifiers

FT Disulfide-bond 25..38

FT Disulfide-bond 28..34

XX W09746581-A1.

PN 11-DEC-1997.

XX 04-JUN-1997; 97WO-AU00351.

XX 05-JUN-1996; 96AU-0000265.

XX (BIOM-) BIOMOLECULAR RES INST LTD.

XX Gorman JJ;

XX WPI; 1998-042117/04.

XX

PT Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PS against Pneumovirus infection
XX
XX Claim 5; Fig 2; 75pp; English.
XX
CC AAW39217-W39234 are fragments of the human respiratory syncytial virus
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to
CC host cells and for characterisation of cell receptors for Pneumoviruses.
CC When the fragments are used in combination with existing vaccines, they
CC may allow a reduction in dose, and thus side effects, of the vaccine.
XX
XX Sequence 49 AA;
SQ

Query Match 100.0%; Score 288; DB 19; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.2e-28;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNDFHFVEFVPCISCSNNPTCWAICKRIPNKKPGKK 49
DB 1 KORQNKPPSKPNDFHFVEFVPCISCSNNPTCWAICKRIPNKKPGKK 49

RESULT 2
AAW39244
ID AAW39244 standard; peptide; 49 AA.
AC AAW39244;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human RSV G protein fragment (aa. 149-157) derivative #1.
XX
DE Human RSV G protein fragment (aa. 149-157) derivative #1.
XX
G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
OS Human respiratory syncytial virus.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetylated"
FT Disulfide-bond 25..38
FT Disulfide-bond 28..34
FT Modified-site 49 /note= "C-terminal amide"
FT
PN WO9746581-A1.
XX
PD 11-DEC-1997.
XX
PF 04-JUN-1997; 97WO-AU00351.
XX
PR 05-JUN-1996; 96AU-0000265.
XX
PA (BIOM-) BIOMOLECULAR RES INST LTD.
XX
PI Gorman JJ;
XX
DR WPI; 1998-042117/04.
XX
PT Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection
XX
XX Example 4; Fig 12; 75pp; English.
XX
XX AAW39244-W39252 are derivatives of the human respiratory syncytial virus
XX (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to
CC host cells and for characterisation of cell receptors for Pneumoviruses.
CC When the fragments are used in combination with existing vaccines, they
CC may allow a reduction in dose, and thus side effects, of the vaccine.
XX
XX Sequence 49 AA;
SQ

CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to
CC host cells and for characterisation of cell receptors for Pneumoviruses.
CC When the fragments are used in combination with existing vaccines, they
CC may allow a reduction in dose, and thus side effects, of the vaccine.
XX
XX Sequence 49 AA;
SQ

Query Match 100.0%; Score 288; DB 19; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.2e-28;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNDFHFVEFVPCISCSNNPTCWAICKRIPNKKPGKK 49
DB 1 KORQNKPPSKPNDFHFVEFVPCISCSNNPTCWAICKRIPNKKPGKK 49

RESULT 3
AAW39248
ID AAW39248 standard; peptide; 49 AA.
XX
AC AAW39248;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human RSV G protein fragment (aa. 149-157) derivative #5.
XX
KW G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
OS Human respiratory syncytial virus.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal fitc group"
FT Disulfide-bond 25..38
FT Disulfide-bond 28..34
FT Modified-site 49 /note= "C-terminal amide"
FT
PN WO9746581-A1.
XX
PD 11-DEC-1997.
XX
PF 04-JUN-1997; 97WO-AU00351.
XX
PR 05-JUN-1996; 96AU-0000265.
XX
PA (BIOM-) BIOMOLECULAR RES INST LTD.
XX
PI Gorman JJ;
XX
DR WPI; 1998-042117/04.
XX
PT Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection
XX
XX Example 4; Fig 12; 75pp; English.
XX
XX AAW39244-W39252 are derivatives of the human respiratory syncytial virus
XX (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to
CC host cells and for characterisation of cell receptors for Pneumoviruses.
CC When the fragments are used in combination with existing vaccines, they
CC may allow a reduction in dose, and thus side effects, of the vaccine.
XX
XX Sequence 49 AA;
SQ


```
DE G protein.
XX Vaccine.
XX Human respiratory syncytial virus (HRSV).
XX
XX W08704185-A.
XX
XX 16-JUL-1987.
XX
XX 23-DEC-1986; 86WO-US02756.
XX
XX 14-JAN-1986; 86US-0818740.
XX
XX (UYN-) UNIV OF N CAROLINA.
XX (WERTZ/) WERTZ G W.
XX (WERTZ/) WERTZ G W.
XX
XX WPI; 1987-206300/29.
XX N-PSDB; AAN70784.
XX
XX Vaccines for human respiratory virus - comprising proteins or
XX fragment encoded by a DNA sequence coding for human respiratory
XX syncytial virus proteins.
XX
XX Disclosure; Chart 13; 57pp; English.
XX
XX A novel plasmid which comprises a DNA sequence encoding this
XX protein, and the protein itself, are claimed, for use as HRSV
XX vaccines. The vaccine can be administered to pregnant women or to
XX women of child bearing age to stimulate maternal antibodies.
XX Infants can also be vaccinated at 2-3 months of age.
XX
XX Sequence 298 AA;
XX
XX Query Match 100.0%; Score 288; DB 8; Length 298;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-27;
XX Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KORQKPPSKPNDHFHFEVFNVPSCSNNPTCWAICKRIPNKKPKKK 49
XX |||||||||||||||||||||||||||||||||||||||||||||||
XX 149 KORQKPPSKPNDHFHFEVFNVPSCSNNPTCWAICKRIPNKKPKKK 197
XX
XX RESULT 7
XX AAR25302
XX ID AAR25302 standard; Protein; 298 AA.
XX
XX AC AAR25302;
XX
XX 03-MAR-1993 (first entry)
XX
XX HSRV glycoprotein G (gpG).
XX
XX Vaccine; human respiratory syncytial virus; HRSV; F; G; 22K; 9.5K;
XX major capsid protein; N.
XX
XX Human respiratory syncytial virus strain A2.
XX
XX US5149650-A.
XX
XX 22-SEP-1992.
XX
XX 14-JAN-1986; 86US-0818740.
XX
XX 14-JAN-1986; 86US-0818740.
XX 13-JUL-1986; 88US-0218737.
XX
XX (UYN-) UNIV NORTH CAROLINA.
XX
XX Collins PL, Wertz GW;
XX
XX WPI; 1992-340247/41.
```

```
DR N-PSDB; AAQ29623.
XX
XX Vaccines for human respiratory virus - include structural genes
XX coding for native structural viral proteins and immunogenic
XX fragments
XX
XX Disclosure; Page 18; 21pp; English.
XX
XX The sequences of mRNA encoding HRSV structural proteins are given in
XX CC AAQ29622-26. The proteins are F, G, 22K, 9.5K and major capsid
XX CC protein N. The sequences and encoded proteins are useful for
XX CC preparing vaccines against HRSV. The vaccines can be used to confer
XX CC immunity against respiratory tract infections on human subjects.
XX
XX Sequence 298 AA;
XX
XX Query Match 100.0%; Score 288; DB 13; Length 298;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-27;
XX Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KORQKPPSKPNDHFHFEVFNVPSCSNNPTCWAICKRIPNKKPKKK 49
XX |||||||||||||||||||||||||||||||||||||||||||||||
XX 149 KORQKPPSKPNDHFHFEVFNVPSCSNNPTCWAICKRIPNKKPKKK 197
XX
XX RESULT 8
XX AAW47605
XX ID AAW47605 standard; Protein; 298 AA.
XX
XX AC AAW47605;
XX
XX 11-JUN-1998 (first entry)
XX
XX HRSV glycoprotein G.
XX
XX HRSV; glycoprotein F; gpF; glycoprotein G; gpG; vaccine.
XX
XX Human respiratory syncytial virus.
XX
XX US5716823-A.
XX
XX 10-FEB-1998.
XX
XX 12-MAY-1997; 97US-0854783.
XX
XX 13-JUL-1988; 88US-0218737.
XX 14-JAN-1986; 86US-0818740.
XX 23-DEC-1986; 86WO-US02756.
XX 11-JUN-1992; 92US-0897171.
XX 12-MAY-1997; 97US-0854783.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Collins PL, Wertz GW;
XX
XX WPI; 1998-144802/13.
XX N-PSDB; AAV18736.
XX
XX Production of human respiratory syncytial virus glyco-protein F or G
XX - by culturing eukaryotic host cells transfected with corresponding
XX DNA
XX
XX Example 1; Columns 27-28; 17pp; English.
XX
XX The present sequence was used in the development of a novel method
XX CC for the production of human respiratory syncytial virus (HRSV)
XX CC glycoprotein F (gpF) or glycoprotein G (gpG). The method comprises
XX CC culturing eukaryotic host cells transfected with an isolated DNA
XX CC sequence encoding HRSV gpF or gpG. The gp can be used to prepare
XX CC vaccines against HRSV.
XX
XX Sequence 298 AA;
```

Query Match 100.0%; Score 288; DB 19; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.4e-27;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNDHFHFEVFNFCVCSNNTPTCWAICKRIPNKKPGKK 49
 Db 149 KORQKPPSKPNDHFHFEVFNFCVCSNNTPTCWAICKRIPNKKPGKK 197

RESULT 9
 AAU74676
 ID AAU74676 standard; Protein; 298 AA.
 XX AC AAU74676;
 XX AC
 XX DT 09-APR-2002 (first entry)
 XX DE Respiratory syncytial virus G protein.
 XX KW RSV; G protein; heavily glycosylated protein; antianaemic; antiviral;
 XX KW vaccine; gene therapy; paramyxovirus; Sendai virus; PMV;
 XX KW antiviral chemotherapeutic compound; humoral response;
 XX KW cellular immune response; hpiv; paediatric respiratory disease;
 XX KW globulin gene transfer; sickle cell disease; beta-thalassaemia;
 XX KW human immunodeficiency virus infection; HIV.
 XX OS Human respiratory syncytial virus.
 XX PN WO200192548-A2.
 XX PD 06-DEC-2001.
 XX PF 22-MAY-2001; 2001WO-US16610.
 XX PR 01-JUN-2000; 2000US-208701P.
 XX PA (SUUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 XX PI Portner A, Takimoto T;
 XX DR WPI: 2002-130534/17.
 XX DR N-PSDB; AAS21045.
 XX PT Recombinant Sendai virus useful in vaccines to protect infection by
 PT paramyxoviruses, comprises exogenous nucleic acid encoding
 PT paramyxovirus protein or its antigenic fragment
 XX PS Disclosure; Page 48; 57pp; English.

The invention relates to a recombinant Sendai virus comprising an
 exogenous nucleic acid encoding a paramyxovirus (PMV) protein or its
 antigenic fragment. The virus may be administered in combination
 with an antiviral chemotherapeutic compound. Two or more viruses
 expressing different PMV proteins may be co-administered. Compositions
 comprising the virus are useful for eliciting a humoral and/or
 cellular immune response to a PMV in a mammal, particularly a human.
 Further a recombinant Sendai virus comprising an exogenous nucleic acid
 encoding a second PMV protein is also administered and priming and/or
 boosting humoral or cellular immune response comprises administering
 one or more of a recombinant or isolated PMV protein or its antigenic
 fragment, a DNA vaccine encoding the same, and a non-Sendai viral
 vector encoding a PMV protein. The recombinant virus is useful as an
 effective vaccine against hpiv or RSV (the major causes of paediatric
 respiratory disease) and also to express any gene of
 interest in target cells, providing a positive medical impact on
 impaired cells. Wild-type globulin gene transfer (i.e. gene therapy)
 into stem cells effects a cure for sickle cell disease or beta-
 thalassaemia. The recombinant virus may also prove effective in
 conferring immunity to human immunodeficiency virus (HIV) infection.
 The Sendai virus replicates at level that is high enough to
 induce sufficient immunity, but does not cause any harm to human
 recipient. The present sequence represents a respiratory syncytial
 virus (RSV) G protein (heavily glycosylated protein), a PMV protein

CC suitable for expression by the recombinant virus of the invention.
 XX SQ Sequence 298 AA;
 Query Match 100.0%; Score 288; DB 23; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.4e-27;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNDHFHFEVFNFCVCSNNTPTCWAICKRIPNKKPGKK 49
 Db 149 KORQKPPSKPNDHFHFEVFNFCVCSNNTPTCWAICKRIPNKKPGKK 197

RESULT 10
 AAP90441
 ID AAP90441 standard; protein; 681 AA.
 XX AC AAP90441;
 XX DT 01-NOV-1989 (first entry)
 XX DE Chimeric human respiratory syncytial virus glycoproteins F and G.
 XX KW Chimeric polypeptide; human respiratory syncytial virus;
 XX KW protein F; protein G; vaccine.
 XX OS Human respiratory syncytial virus.
 XX PN WO8905823-A.
 XX PD 29-JUN-1989.
 XX PF 31-OCT-1988; 88WO-US03784.
 XX PR 23-DEC-1987; 87US-0137387.
 XX PA (UPJO) UPJOHN CO.
 XX PI Wathen M;
 XX DR WPI: 1989-206593/28.
 XX PT Chimeric human respiratory syncytial virus polypeptides(s)
 PT - contg. immunogenic fragments from HRSV glycoproteins
 PT F and G, for vaccine prodn.
 XX PS Claim 3; page 47-48; 50pp; English.
 XX CC Chimeric polypeptide contg. a signal sequence and one or more
 CC immunogenic fragments from both human respiratory syncytial virus
 CC glycoproteins F and G. Can be used in vaccines. Hosts are, eg
 CC E. coli, Chinese hamster ovary cells, murine C127 cells and
 CC S. frugiperda.
 XX SQ Sequence 681 AA;
 Query Match 100.0%; Score 288; DB 10; Length 681;
 Best Local Similarity 100.0%; Pred. No. 3.2e-27;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNDHFHFEVFNFCVCSNNTPTCWAICKRIPNKKPGKK 49
 Db 543 KORQKPPSKPNDHFHFEVFNFCVCSNNTPTCWAICKRIPNKKPGKK 591

RESULT 11
 AAW39218
 ID AAW39218 standard; peptide; 49 AA.
 XX AC AAW39218;
 XX DT 27-AUG-1998 (first entry)
 XX

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DE Human RSV A subtype G protein fragment (aa 149-157) strain long A.
XX
KW G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
OS Human respiratory syncytial virus.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 25..38
FT Disulfide-bond 28..34
XX
PN WO9746581-Al.
XX
PD 11-DEC-1997.
XX
PF 04-JUN-1997; 97WO-AU00351.
XX
PR 05-JUN-1996; 96AU-0000265.
XX
PA (BIOM-) BIOMOLECULAR RES INST LTD.
XX
PI Gorman JJ;
XX
DR WPI; 1998-042117/04.
XX
PT Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection
XX
PS Claim 5; Fig 2; 75pp; English.
XX
CC AAW39217-W39234 are fragments of the human respiratory syncytial virus
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to
CC host cells and for characterisation of cell receptors for Pneumoviruses.
CC When the fragments are used in combination with existing vaccines, they
CC may allow a reduction in dose, and thus side effects, of the vaccine.
XX
SQ Sequence 49 AA;
XX
Query Match 99.0%; Score 285; DB 19; Length 49;
Best Local Similarity 98.0%; Pred. No. 5.3e-28;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORQNKPPSKPNNDHFVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
DB 1 KORQNKPPSKPNNDHFVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
RESULT 12
AAW39219
ID AAW39219 standard; peptide: 49 AA.
XX
AC AAW39219;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human RSV A subtype G protein fragment (aa. 149-157) strain A642.
XX
KW G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
OS Human respiratory syncytial virus.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 25..38
FT Disulfide-bond 28..34
XX
PN WO9746581-Al.
XX

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PD 11-DEC-1997.
XX
PF 04-JUN-1997; 97WO-AU00351.
XX
PR 05-JUN-1996; 96AU-0000265.
XX
PA (BIOM-) BIOMOLECULAR RES INST LTD.
XX
PI Gorman JJ;
XX
DR WPI; 1998-042117/04.
XX
PT Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection
XX
PS Claim 5; Fig 2; 75pp; English.
XX
CC AAW39217-W39234 are fragments of the human respiratory syncytial virus
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to
CC host cells and for characterisation of cell receptors for Pneumoviruses.
CC When the fragments are used in combination with existing vaccines, they
CC may allow a reduction in dose, and thus side effects, of the vaccine.
XX
SQ Sequence 49 AA;
XX
Query Match 99.0%; Score 285; DB 19; Length 49;
Best Local Similarity 98.0%; Pred. No. 5.3e-28;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORQNKPPSKPNNDHFVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
DB 1 KORQNKPPSKPNNDHFVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
RESULT 13
AAW39221
ID AAW39221 standard; peptide: 49 AA.
XX
AC AAW39221;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human RSV A subtype G protein fragment (aa. 149-157) strain A6256.
XX
KW G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
OS Human respiratory syncytial virus.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 25..38
FT Disulfide-bond 28..34
XX
PN WO9746581-Al.
XX
PD 11-DEC-1997.
XX
PF 04-JUN-1997; 97WO-AU00351.
XX
PR 05-JUN-1996; 96AU-0000265.
XX
PA (BIOM-) BIOMOLECULAR RES INST LTD.
XX
PI Gorman JJ;
XX
DR WPI; 1998-042117/04.
XX
PT Peptide(s) derived from specific region of respiratory syncytial

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PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection

PS Claim 5; Fig 2; 75pp; English.

XX
XX
CC AAW39217-W39234 are fragments of the human respiratory syncytial virus
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to
CC host cells and for characterisation of cell receptors for Pneumoviruses.
CC When the fragments are used in combination with existing vaccines, they
CC may allow a reduction in dose, and thus side effects, of the vaccine.

SQ Sequence 49 AA;

Query Match 99.0%; Score 285; DB 19; Length 49;
Best Local Similarity 98.0%; Pred. No. 5.3e-28;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KORQNKPPSKPNDFHFEVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 49

Db 1 KORQNKPPSKPNDFHFEVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 49

RESULT 14

AAW39222
ID AAW39222 standard; peptide: 49 AA.

XX
AC AAW39222;

XX
DT 27-AUG-1998 (first entry)

XX Human RSV A subtype G protein fragment (aa. 149-157) strain A6190.

XX G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.

XX Human respiratory syncytial virus.

XX Key Location/Qualifiers
FH Disulfide-bond 25..38
FT Disulfide-bond 28..34

XX WO9746581-A1.

XX 11-DEC-1997.

XX 04-JUN-1997; 97WO-AU00351.

XX 05-JUN-1996; 96AU-0000265.

XX (BIOM-) BIOMOLECULAR RES INST LTD.

XX Gorman JJ;

XX WPI; 1998-042117/04.

XX Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection

PS Claim 5; Fig 2; 75pp; English.

XX
XX
CC AAW39217-W39234 are fragments of the human respiratory syncytial virus
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to
CC host cells and for characterisation of cell receptors for Pneumoviruses.
CC When the fragments are used in combination with existing vaccines, they

CC may allow a reduction in dose, and thus side effects, of the vaccine.
XX
SQ Sequence 49 AA;

Query Match 99.0%; Score 285; DB 19; Length 49;
Best Local Similarity 98.0%; Pred. No. 5.3e-28;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KORQNKPPSKPNDFHFEVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 49

Db 1 KORQNKPPSKPNDFHFEVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 49

RESULT 15

AAW39223
ID AAW39223 standard; peptide: 49 AA.

XX
AC AAW39223;

XX
DT 27-AUG-1998 (first entry)

XX Human RSV A subtype G protein fragment (aa. 149-157) strain A5857.

XX G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.

XX Human respiratory syncytial virus.

XX Key Location/Qualifiers
FH Disulfide-bond 25..38
FT Disulfide-bond 28..34

XX WO9746581-A1.

XX 11-DEC-1997.

XX 04-JUN-1997; 97WO-AU00351.

XX 05-JUN-1996; 96AU-0000265.

XX (BIOM-) BIOMOLECULAR RES INST LTD.

XX Gorman JJ;

XX WPI; 1998-042117/04.

XX Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection

PS Claim 5; Fig 2; 75pp; English.

XX
XX
CC AAW39217-W39234 are fragments of the human respiratory syncytial virus
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to
CC host cells and for characterisation of cell receptors for Pneumoviruses.
CC When the fragments are used in combination with existing vaccines, they
CC may allow a reduction in dose, and thus side effects, of the vaccine.

SQ Sequence 49 AA;

Query Match 99.0%; Score 285; DB 19; Length 49;
Best Local Similarity 98.0%; Pred. No. 5.3e-28;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KORQNKPPSKPNDFHFEVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 49

Db 1 KORQNKPPSKPNDFHFEVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 49

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